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Query Match Best Local S Matches 861	ORIGIN	CDS	source	FEATURES	TITLE JOURNAL	AUTHORS	SOURCE	RESULT 1 AX392419 LOCUS DEFINITION ACCESSION VERSION
y Match 100.0%; Score 861; DB 6; Length 861; Local Similarity 100.0%; Pred. No. 1.4e-126; hes 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/codon_start=1 /protein_id="CAD29006.1" /brotein_id="CAD29006.1" /db_xref="GI:19700735" /db_xref="GI:19700735" /translation="MHRLMGVNSTAAAAAGQPNVSCTCNCKRSLFQSMEITELEFVQI /translation="MHRLMGVNSTAAAAAGQPNVSCTCNCKRSLFQSMEITELEFVQI /translation="MHRLMGVNSTAAAAAGQPNVSCTCNCKRSLEGSEGCLMPSESTYVSGN IIIVVNMVMVVVITCLLSHYKLSARSFISRHSQGFRREDLESEGCLMPSESTYSGN GIPEPQVVAPRFPTDRLAVPFPAQREEFRHFTPTSJCLMDESARLGGPCFPSSNSGISATC YGSGGRMEGSPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWS KEKDKQKGHPL"	/organisms buytens /mol_type="unassigned DNA" /db_xref="taxon:9606" 1.	1861	Location/Qualifiers	Diagnosis and treatment of cardiovascular conditions Diagnosis and treatment of cardiovascular conditions Patent: WO 0216416-A 3 28-FEB-2002; THE BUTCHAM AND WOMEN'S 1050PTBAL. TNC. (US): PRIZER INC. (US)	l Lee,R.T., Landschulz,K.T., Kennedy,S.P., Thompson,J.F. and Thri T.G.	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	AX392419 861 bp DNA linear PAT 23-MAR-2002 Sequence 3 from Patent WO0216416. AX392419 AX392419.1 GI:19700734

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(DE); Dahi
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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Target genes for the diagnosis and treatment
Patent: WO 2004038020-A 109 06-MAY-2004;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Hinzmann, B., Dahl, E., Rosenthal, A., Specht, T., Schmitt, A., Beckmann, G., Bruemmendorf, T., Kinnemann, H., Roepcke, S., He. Xinzhong, L., Pilarsky, C. and Staub, E. Human nucleic acid sequences obtained from prostatic carcin Patent: WO 2004076614-A 71 10-SEP-2004; Hinzmaran, Bernd'(DE); Dahl, Edgar (DE); Rosenthal, Andre (Specht, Thomas (DE); Schmitt, Armin (DE)
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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Patent: WO 2004113571-A 166 29-DEC-2004;
Exonhit Therapeutics S.A. (FR)
Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Primates; Cata
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                                  AGGCTGGGCGGCCCCTGCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGC
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/db_xref="taxon:9606"
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1 (bases) 1 to 4839)
Rae, F. K., Hooper, J. D., Nicol, D. L. and Clements, J. Characterization of a novel gene, STAGI/PMEPA1, urenal cell carcinoma and other solid tumors
Mol. Carcinog. 32 (1), 44-53 (2001)
                                                                                                                                                                       Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A. Direct Submission
Submitted (14-SEP-2000) Centre for Molecular Biotechnology, Queensland University of Technology, 2 George St, Brisbane, 4001, Australia
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/chromosome="20"
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Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGCCGCCGGCAGCCCAATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG
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                                                                                                           TACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACCTGAACCGG
                                                                                                                                       CAGCACGAGATCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCC
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                                                                                                                                                                                                                                                                                                                            CTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGGCG
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                                                                                                                                                                                                                                                                                                                                                                          TTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGC
                                                                                        GTGCCGCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTG
                                                                                                                                                                                                                                  AGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCA
 AGGCTGGGCGGCCCCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGC
             AGGCTGGGCGGCCCCCGCCCCCAGCAGTAACTCGGGCATCAGCGCCAACGTGCTACGGC
                                             GAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="transmembrane, prostate"
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Pred. No. 1.1e-126;
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RESULT 10
AX775889
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Best Local S
Matches 860
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501
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Sequence 15
AX775889
AX775889.1
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                                                                                                                                                                                                                                              860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NP-kB activating gene
Patent: WO 03048202-A 159 12-JUN-2003;
Asahi Kasei Kabushiki Kaisha (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsuda, A. and Muramatsu, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                           Similarity
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CTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGGGG
                 CTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGCGG
                                                          TTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGGTGGTGGTGATCACGTGC
                                                                          TTTGTTCAGATCATCATCATCGTGGTGGTGATGGTGATGGTGGTGGTGATCACGTGC
                                                                                                                     TCCTGCACGTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG
                                                                                                                                     TCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG
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nilarity 99.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                     /protein_id="CAE11644.1"
/db_xref="GI:32693608"
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                        KEKDKQKGHPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="unnamed protein
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:32693607
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from Patent WO03048202.
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Pred. No. 2.4e-126;
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                                                                                                                                                                                                                                                                                                                                                      ORGANISM
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki.S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, L., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sancheg, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
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BC015918.1
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1 (bases 1 to 1061)
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                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 29 Row: e Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                    Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
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Submitted (15-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
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The I.M.A.G.E. Consortium (LLNL)
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S Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.

S Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.

Secreted proteins and nucleic acids encoding them

Patent: JP 2002539773-A, 3 26-NOV-2002;

MILLENNIUM PHARMACEUTICALS INC

OS Homo sapiens (human)

PN P 2002539773-A/3

PD 26-NOV-2002

PP 01-MAR-2000 JP 2000602247

PP 01-MAR-1999 US 60/122458

PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHI

PR RASER

PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C

G01N33/15,

G01N33/50,G01N33/53,G01N33/53,G01N33/566,C12N15/00

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted proteins and nucleic acids encoding them FH Key Location/Qualifiers (6)...(761).
TGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCAT
                                                                      GCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAG
                                                                                                                 CGGGGAGGACCCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCA
                                                                                                                                          CGGGGAGCACCCCACCCACCAGGGCCCCTGCAGCCTCCAGCTTCGGGACCCCCGAGCA
                                                                                                                                                                                           GCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCA
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THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 7.4e-110;
0; Mismatches 3;
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Direct Submission
Open CPDR,
Submitted (12-TAN-2000) CPDR,
Submitted (12-TAN-2000) CPDR,
Submitted (12-TAN-1000) CPDR,
Submitted (12-TAN-1000) CPDR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens PMEPA1 protein
AF224278
AF224278.1 GI:9255808
                                                                                                                                                                                                                                                                                                                                                                                                                                             A novel androgen-regulated gene, PMEPA1,
20q13 exhibits high level expression in
Genomics 66 (3), 257-263 (2000)
10873380
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Moul,J.W. and Srivastava,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo.
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                                 Number NP_004329"

/codon_start=1
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/product="PMEPA1 protein"
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LMDSARLGGPCPPSSNGGISATCYGSGGRMEGPPTYSEVIGHYPGSSFQHQQSSGPP
                                                                                                                                                 /note="type 1b transmembrane protein; expression is induced in response to the synthetic androgen, R1881; expression is abundant in, and restricted to, prostate glandular epithelial cells; similar to the predicted protein encoded by sequence deposited at GenBank Access
                         SLLEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL"
                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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                                                                                                                                                                                                                 /gene="PMEPA1"
                                                                                                                                                                                                                                        /gene="PMEPA1"
                                                                                                                                                                                                                                                                   /map="20q13.31-13.33"
/cell_line="LNCaP"
                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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                                                                                                                           Sequence 127 from Patent CS130841 CS130841.1 GI:71792911
OBrntoft, T.F.
Classification of cancer
Patent: WO 2005064009-A 127 14-JUL-2005;
                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                    Homo sapiens (human)
                                                                                                                                                                  CS130841
                                                  Hominidae;
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Homo.

Chordata; Craniata; Vertebrata; Buteleostomi; Euarchontoglires; Primates; Catarrhini;

4538 bp DNA : WO2005064009.

linear

PAT

02-AUG-2005

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Query Match
Best Local Similarity
Matches 762; Conserv
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                     AGAGAGCGCAGCCATCTGGAGCAAAGAGAAAGGATAAACAGAAAAGGACACCCTCTC
                                                          GCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTTCCCAGCACCAGCAGGAG
                                                                                                                                                                                                                       AACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAG
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AGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCCTCTC
                                                                                                 GCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAG
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98.3%;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="transmembrane, pros
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Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C. (
Secreted proteins and nucleic acids encoding them

Secreted proteins and nucleic acids encoding them

Learnest TP 2002539773-A 53 26-NOV-2002;

MILLENNIUM PHARMACEUTICALS INC

OS Homo sapiens (human)
PN JP 2002539773-A/53

PD 26-NOV-2002

PF 01-MAR-2000 JP 2000602247

PF 01-MAR-1999 US 60/122458
PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP,

PI FRASER
PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/0;

G01N33/15,

G01N33/15, G01N33/63 G01N33
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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861
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score greater than and is derived by a Pred. No. is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.

## SUMMARIES

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87.6	87.6	87.6	87.6	87.7	99.8	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
4527	1850	1141	1140	969	1383	4930	4911	4839	4839	4839	4839	4839	4839	4839	4839	4519	1321	864	Query Match Length
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ADL83313	ACC49536	ADB75588	ABK92120	AAA75151	ADC37326	AEB22787	ACN40804	ADW43368	ADU06063	ADR66778	ADR65875	ADM67045	ADP65729	ADP65809	ACC49552	ADX97454	ABK12137	ADN38809	ID
Adi83313 Human and	Acc49536 Tumour-as	Adb75588 Prostate	Abk92120 Prostate	Aaa75151 cDNA enco	Adc37326 Nuclear f	Aeb22787 Human col	Acn40804 Tumour-as	Adw43368 Prostate	Adu06063 Novel bro	Adr66778 Human pro	Adr65875 Human pro	Adm67045 Human hom	Adp65729 Human tra	Adp65809 Human STA	Acc49552 Tumour-as	Adx97454 Pancreati	Abk12137 Human cDN	Adn38809 Cancer/an	Description

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417.4	445.6	460.6	460.6	460.6	462.2	544.4	612.4	712	742.4	752	752.6	752.6	752.6	752.6	752.8	752.8	752.8	753.6	753.6	753.6	753.6	753.6	753.6	754.2	754.2
48.5	51.8	53.5	53.5	53.5	53.7	63.2	71.1	82.7	86.2	87.3	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.5	87.5	87.5	87.5	87.5	87.5	87.6	87.6
812	693	1713	1713	1713	1713	1583	878	1069	1066	4531	1334	1085	1061	806	759	759	759	1140	1140	1140	969	969	969	4538	4527
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AAZ52964	ABK12143	AAA75168	AAA75166	AAA75167	AAA75152	ABS61424	ABK12142	AAI59654	AAI57868	AEB22833	ABZ36103	ADC37324	AAA47429	ACC49537	AD039827	ADH62277	ADF17545	AD039826	ADH62276	AAD60105	AAA75165	AAA75163	AAA75164	AEB22832	ADV85880
Aaz52964 Human pro		CDNA		CUNA	CUNA			Human	Human	3 Huma	Abz36103 Human sec	Adc37324 Nuclear f	Aaa47429 Sequence	Acc49537 Tumour-as	Ado39827 Human PME	Adh62277 Human PME	Human	Human	Human	Human	Aaa75165 cDNA cion		CDNA	nut z	Adv85880 Human ARP

ALIGNMENTS

ADN38809 standard; cDNA; 864 BP

ADN38809;

Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:127. 17-JUN-2004 (first entry)

Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease;

retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.

Homo sapiens.

WO2003042661-A2

22-MAY-2003.

13-NOV-2002; 2002WO-US036810

RESULT 1

ADM39

ID ADM39

XX ADM3

XX ADM3

XX ADM3

XX Canc

XX Huma

KW Hima

KW woun

XX Woln

XX Woln

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PR 29-N

PR 108-0

PR 108-0

PR 108-0

PR 108-0

PR 108-0

PR 29-N

PR 29-N

PR 29-N

PR 108-0

PR 13-NOV-2001; 2001US-0350666P.
21-NOV-2001; 2001US-03343439P.
23-NOV-2001; 2001US-0334393P.
03-DEC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0340376P.
08-JAN-2002; 2002US-0347349P.
10-JAN-2002; 2002US-0347349P.
08-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0355714P.
20-FEB-2002; 2002US-0359077P.
29-MAR-2002; 2002US-0356809P.
04-APR-2002; 2002US-0370710P.
12-APR-2002; 2002US-0370710P.
15-APR-2002; 2002US-0356614P.
05-JUN-2002; 2002US-0396839P.
16-JUL-2002; 2002US-0396839P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     whose expression is upregulated or downregulated in specific cancers or cother diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a comparison of determining the presence or absence of the invention or by detecting a nucleic acid at least 80% identical to those of the invention also relates to expression vectors and host cells comprising a conclusic acid of the invention; antibodies which specifically bind a compression of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and mucleic acids. The nucleic acidis, polypeptides, can important to the conditions such as psoriasis, ischaemia, heart disease, can includies and other conditions such as psoriasis, ischaemia, heart disease, can therosclerosis, inflammatory diseases, autoimmune diseases, retinal consocularistaion syndromes, scarring and uterine fibroids. They may calso be useful in wound healing and in contraception. The present of the invention.
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Best Local Similarity
Matches 861; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID NO 127; 1385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-468649/44.
P-PSDB; ADN38810.
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09-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 864 BP; 173 A; 307 C; 254 G; 130 T; 0 U; 0 Other;
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 CAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGGAGGAGCCCCCACCC
                                                                                       GTGCCGCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTG
                                                                                                                                                           AGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCA
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                                 CAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCC
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2002US-0409450P.
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R, Watson SR,
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Pred. No. 2.6e-167;
Mismatches 0;
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Wilson I
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RESULT 2
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AX BHUMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor
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     Claim
                                              Novel nucleic acid molecule encoding Mechanically Induced Vascular Receptor-1 polypeptide, useful for treating cardiovascular diseases
                                                                                                                                                                                                                                                                                                                                 22-AUG-2000; 2000US-0227159P.
                                                                                                                                                                                                                                                                                                                                                                             21-AUG-2001; 2001WO-US026089
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                                                                                                                                                                                                      Lee RT,
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2; Page 87-88; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              failure.
                                                                                                                                                                                                                                                    BRIGHAM & WOMENS HOSPITAL INC. PFIZER INC.
                                                                                                                              AAU78231
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/product= "MIVR-1"
/note= "This region
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                                                                                                                                                                                                   Thompson
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                                                      cardiovascular diseases.
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The invention relates to an isolated nucleic acid molecule encoding a CC Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having CC cardiac cell anti-apoptotic activity and fragments of it provided they CR are not identical to Genhank sequences A1761441.1, A1594390, NM 004338 CC and AQ177461. Also included are expression vectors, host cells, the MIVR-1 contacting cardiac cell anti-apoptotic activity with a candidate CR amolecule having cardiac cell anti-apoptotic activity with a candidate CR CRX-1, VDUP-1, BTG-2 and TIS-11d or its expression product, determining CR CRX-1, VDUP-1, BTG-2 and TIS-11d or its expression product, determining CR CRX-1, VDUP-1, BTG-2 and TIS-11d or its expression product, determining CR condulator. The cardiac cell anti-apoptotic molecules and nucleic acids of the invention are useful for treating, diagnosing and monitoring CR progression of such diseases and disorders as characterised by increased CR apoptotic cell-death of vascular endothelial cells e.g. cardiac CR hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart CR failure. The present sequence encodes human MIVR-1
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      The invention relates to a novel human nucleic acid sequence of the CC pancreas and its encoded protein. The invention further comprises: CC proteins and peptides, preferably isolated, that contain a sequence ce encoded by the novel nucleic acid; and methods for diagnosis and contain a sequence ce in the protein or its DNA, including: an antisense oligonucleotide, short ce interfering RNA or ribozyme directed against the pancreatic protein, an cc organic molecule, particularly having a molecular weight below 5000, ce especially 300, that binds to the pancreatic DNA, an aptamer or ce (monoclonal) antibody, preferably human or humanized, that binds to the pancreatic DNA, an aptamer or ce monoclonal antibody, any of which may be derivatized with a reporter compout, cyrotoxic compound, immunostimulant and/or radioisotope. The novel fuman pancreatic proteins and their encoding DNA, have cytostatic compound, immunostimulant and/or radioisotope. The novel cartivity. The novel sequences are useful for inhibiting transcription cartivity. The novel sequences are useful for inhibiting transcription condours the proteins of the invention. Note: This sequence is not shown in the specification, it has been electronically downloaded from a DVD-rom provided with this specification by the European Patent confirms.
is not from a Office.
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) PILARSKY C.
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Pred. No. 3.3e-167;
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03-APR-2002;
19-AUG-2002;
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Williams 1
                                                                                                                                                                                                                                                                              ACC49493 to ACC49552 encode the human tumour-associated antigenic target (TAT) proteins given in ABP97175 to ABP97234. The present invention describes an isolated antibody that binds to a polypeptide having at least 80 % sequence identity to any of the 60 150-800 residue amino acid sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking its associated signal peptide, encoded by any of the 60 2000-3000 base pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have cytostatic activity. The antibody can be used for treating or diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast cancer, colon cancer, oversian cancer, prostate adenocarcinomas, renal
                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibodies against tumor-associated antigenic target polypeptide, useful for treating or diagnosing tumors or cancers in mammals, e.g. prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
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The invention relates to a novel method for diagnosing and analysing coutoimmune disease or arthritides. The method comprises obtaining a containing mRNA, analysing gene expression using the mRNA cut that results in a gene expression signature of the mRNA corrections in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention conformation of further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis; in a mammal; an containing of a diagnosis of rheumatoid arthritis; in a mammal; an containing specific for rheumatoid arthritis; diagnosis or caray or gene chip, specific for rheumatoid arthritis; diagnosis or induced arthritis. The compositions of the invention have the following cartivities in an reducing the specific for rheumatoid arthritis; diagnosis or candidate drug in vitro for the treatment of collagentiduced arthritis. The compositions of the invention have the following activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic, cantiduced arthritis, antionisment of the present invention are useful for diagnosing and treating autoimmune disease or arthritis, fibrositis, and an immune disease caused by an infectious agent. This polynucleotide represents a DNA sequence relating to the genes used in the analysis and cot shown in the specification. It has been supplied in an electronic format from WIPO.
Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating theumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
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Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match Best Local ( Matches 861;

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                  Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia doubt
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            gout..
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Disclosure; Page; 56pp; English

Conservation in a year expression signature to diagnose or analyse the autoimmune disease correlates in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention of further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis; in a mammal content than a mouse; diagnosis of rheumatoid arthritis; diagnosis or array or gene chip, specific for rheumatoid arthritis; diagnosis or consultate of autoimmune disease or rheumatoid arthritis; diagnosis or conduced arthritis; and reducing the symptoms associated with collagentinduced arthritis. The compositions of the invention have the following activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic, antigout, antiarthritis, dermatoid arthritis, and reducing the greening the control of the present invention have the following contivities: immunosuppressive, antirheumatic, and immunomodulatory. The control of the present invention are useful for the immuned disease or arthritis, supus, antylosing spondylitis, fibrositis, and an immuned disease caused by an infectious agent. This sequence is control shown in the specification. It has been supplied in an electronic format from MIPO. The invention relates to a novel method for diagnosing and analysing autoimmune disease or archritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNJ that results in a gene expression signature of the mRNA, and using that format from WIPO. the mRNA

Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match
Best Local Similarity
Matches 861; Conserv

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Score 861; DB 11; Pred. No. 3.3e-167; Mismatches 0;

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ATCTTCGACAGTGACCTGATGGATAGTGCC 600	a gagtogotgogogoacococoaacagaacoatcttcgacagtgacotgatggatagtgoco	541	ş
BACCCCGAGCAGCAGCTGGAACTGAACCGG 860	1 TACCAGGGCCCCTGCACCTCCAGCTTCGGGACCCCGAGCAG	801	ర్జ
ARCCCCGAGCAGCAGCTGGAACTGAACCGG 540	TACCAGGGCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGG	481	Ş
rcgcTgTCAGACGGGGAGGAGCCCCCACCC 800	1 CAGCACGAGATCGACCCACCCACCCACCCTGTCAGACGGGGAGGAGCCCCCACCC	741	Д
CGCTGTCAGACGGGGAGGAGCCCCCACCC 480	2 CAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGGAGCCCCCACCC	421	ş
DACCGCTTCCAGCCCACCTATCCGTACCTG 740	1 GTGCCGCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTG	681	망
PACCGCTTCCAGCCCACCTATCCGTACCTG 420	TGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCAGCGCTTCCAGCCCACCTATCCGTACCTG	361	Ş
3CCCCGCCTCGGCCCACCGACCGCCTGGCC 680	1 GGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCG	621	В
360	gcaacggaarcccagagccgcaggretacgcccgccrcgcccgcccaccgaccgccrggcc	301	Ş
GCCTGTGGCCCTCGGAGAGCACAGTGTCA 620	1 AGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCT	561	Дb
GCCTGTGGCCCTCGGAGAGCACAGTGTCA 300	AGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCTGGAGAGCACAGTGTCA	241	Ş
CCTTCATCAGCCGGCACAGCCAGGGGCGG 560	1 CTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGCGG	501	망
CCTTCATCAGCCGGCACAGCCAGGGGCGG 240	TGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGCCGG	181	Ś
ATGATGGTGATGGTGGTGATCACGTGC 500	1 TTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGATCACGTGC	441	망
	TTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGC	121	8
TCCAGAGCATGGAGATCACGGAGCTGGAG 440	1 TCCTGCACGTGCAAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG	381	뮍
TCCAGAGCATGGAGATCACGGAGCTGGAG 120	TCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG	61	γQ
CCGCCGCCGCCGGCAGCCCAATGTC 380	1 ATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGCCGGGCAGCCCAATGTC	321	Ъ
	ATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGCCGGGCAGCCCAATGTC	1	8

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This invention relates to a novel method for identifying genes that are over-expressed in adipose tissue and as such it provides targets for anti-
-obesity pharmaceutical compositions. Specifically, it refers to a high mobility group I-C protein (HMGI-C) that is associated with obesity and is epistatic to leptin, furthermore, it refers to the ob gene where an autosomal recessive trait is linked to obesity and diabetes. The present invention describes performing differential gene expression analysis between the white adipose tissue (MAT) or stromal vascular tissue (SVT) of any two different mice selected from a group consisting of wild-type, HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using this method novel nucleotides and the encoded proteins thereof were
                                                                                                                                                                                                                                                                                            Identifying adipocyte specific genes, useful for treating obesity or diabetes, and for identifying drug targets, by differential gene expression analysis between adipose tissue or stromal vascular tissue mice of different genotypes.
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Query Match
Best Local Sim
Matches 861;
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No. 3.3e-167;
1133 T; 0 U; 0 Other;
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RESULT 8
This invention describes novel cytostatic polynucleotide and polypeptide concerses which can be used in a method for diagnosing prostatic cancer. Or the risk of developing prostatic cancer. Diagnosis is based on the risk of developing prostatic cancer. Diagnosis is based on the risk of developing prostatic cancer. Diagnosis is based on the risk of developing for inhibitors of the sequences in compounds that bind are consumed the sequences of the sequence by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that the sequence patients, or subjects at risk, were incubated from the sequence of the second antibody; streptavidin-conjugated horseradish the sequence of the second antibody; streptavidin-conjugated horseradish the sequence of the sequence o
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Schmitt A,
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14-MAY-2003; 2003DE-01022134
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ROSENTHAL A.
HERMANN K.
PILARSKY C.
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Beckmann G,
, Staub E;
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polypeptide sequences used in the method
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orf T, Kinnemann H,
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ADR66778 standard; DNA; 4839

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RESULT 9

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This invention describes novel cytostatic polynucleotide and polypeptide cor the risk of developing prostatic cancer. Diagnosing prostatic cancer cancer. Inagnosis is based on contermining over transcription or over expression of the sequences in compostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are consustances involves a binding assay, any compounds that bind are consustances involves a binding assay, any compounds that bind are consustances involves a binding assay, any compounds that bind are consustances involves a binding assay, any compounds that bind are consustance in the polypeptide of the reporter indicates the presence of two predetermined minimum level of the reporter indicates the presence of two predetermined principles and consumer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotype, non-human consumer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotype, non-human concordinal antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or concers by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that concers and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of opolymucleotide and polypeptide sequences used in the method of the polymucleotide and polypeptide sequences used in the method of the
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) DAHL E.
) ROSENTHAL A.
) HERMANN K.
) PILARSKY C.
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           Novel bronchial cancer-associated human
                                   27-JAN-2005
                                                           ADU06063
                                                                                   ADU06063
                                                                                   standard;
                                    (first entry)
                                                                                   DNA;
                                                                                   4839
            gene SeqID285
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Query Match Best Local Similarity

100.0%;

Score 861; Pred. No. 3

.; DB 13; 3.3e-167;

Length 0 U; 0 Other

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Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel isolated nucleic acid associated with Crown prising 489 defined sequences given in the specification. The invention may be useful for the production of compounds with a cytostatic activity through the inhibition of expression or activity of tumour-associated proteins. The novel DNA sequences and the proteins/peptides encoded by them are used for detecting bronchial cancer or determining the risk of developing it and to screen for specific binding partners of the DNA or protein sequences, where the binding partners are potentially useful as agents for treating or diagnosing bronchial cancer. The DNA or protein sequences can also be used for prognosis, detection of metastases and for secondary treatment (of tumours that have been stabilised or are no longer detectable). Concercing abnormal expression of the DNA sequences provides early changes is of bronchial cancers. The present sequence is that of a novel bronchial cancer-associated human gene sequence of the invention.
                                                                                                                                                                                                                                                                                                                                Query Match
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Matches 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid, and derived proteins, useful for diagnosis of bronchial cancer and in screening for therapeutic and diagnostic agents.
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Li X, Roepc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 285; 1381pp; German
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              AGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGAGCACAGTGTCA
                                                                                                                        CTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGCGG
                                                                                                                                                                                 TTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGATCACGTGC
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AGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCA
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                                         New isolated nucleic acid sequence that is expressed by human prostate cancer cells, useful as target for treating, preventing and/or diagnosing cancers, particularly prostate cancer.
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Claim 1; SEQ

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NO 166; 198pp; English

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                                                         CTCCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGAT 840
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                                                                                                                                 GGGTCCTTCCTTCCAGCAGCAGCAGAGAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGG
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 AAACAGAAAGGACACCCTCTC 861
                                                                                                                                                                                                                                                             AGGCTGGGCGGCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGC
                                      CTCCACCACACACACCCCCCCCCCCCAGAGAGCCCAGCCATCTGGAGCAAAGAGAAGGAT
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Pred. No. 3.3e-167;
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TCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG ATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGGCCAGCCCAATGTC Query Match Best Local S Matches 861

Similarity

100.0%;

Score 861; Pred. No. 3

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RESULT 12
ACN40804
The invention relates to human tumour-associated antigenic target (TAT) copypeptides, and their related nucleic acids. The TAT polypeptides are coverexpressed in cancer tissues compared to normal tissues, and may thus coverexpressed in cancer tissues compared to normal tissues, and may thus coverexpressed in cancer tissues compared to normal tissues, and may thus covered as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide copypeptides; expression vectors and host cells comprising a TAT nucleic color antibody specific for a TAT polypeptide; a peptide or organic conlecule which binds to a TAT polypeptide; apptide or organic concerule which binds to a TAT polypeptide; and proteins comprising a concerule cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful concreased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder colorectal cancer, melanoma and leukaemia. TAT nucleic acids may further be cused as hybridisation probes, in chromosome and gene mapping, in corpresents a TAT nucleic acid of the invention corporates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New tumor-associated antigenic target polypeptides and nucleic useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
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RESULT 13
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immune disorder; neoplasm; colon tumor; gastrointestinal disease;
adenocarcinoma; carcinoma; screening; diagnostic; prognostic;
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Comprising: (a) obtaining a sample from the cancer is determined by a method of cancer, the sample comprising gene expression products, the presence candor amount of which forms a pattern that is indicative of the cancer: (b) determining the pattern, and obtaining an indicative of the cancer: (c) determining the pattern, and obtaining an indication of the cancer: (d) determining the pattern, and obtaining an indication of the groducts forming the pattern, and obtaining an indication of the cancer: (d) determining the pattern, and obtaining an indication of the cancer: (e) the individual based on step (b). At least one or two of the gene expression products forming a pattern used to determine the cancer of in the individual based on step (b). At least one or two of the gene expression products forming a pattern used to determine the cancer of the selected individually from any of the 134 genes comprising 367-7850 (c) are selected individually from any of the 134 genes comprising 367-7850 (c) a method for treating an individual, a method for reducing malignancy of a cell; a method for producing maliphancy of a cell; a method for producing maliphancy of the cell from a biological tissue; pharmaceutical composition, for classification of cancer in an individual having contracted cancer. (c) comprising at least one marker capable of determining the microsatellite status and the prognostic marker; where the microsatellite status and the prognostic composition for the treatment of a cancer in a nimal tissue. The method above is useful for probactions, a method is cancer, i.e. colon cancer, e.g. on adenocarcinoma, a carcinoma, a carcinoma, a sarcoma, and/or a lymphoma. The present sequence represents a colon cancer-associated gene used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-DEC-2003;
24-JAN-2004;
07-APR-2004;
26-NOV-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of classifying the cancer in an individual having contracted cancer, which comprises determining the microsatellite status of the tumor. The microsatellite status or the
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    03-DEC-2002; 2002WO-JP012644
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                                                                         The present invention relates to novel proteins and their coding sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-kappaB). The proteins and their coding sequences are useful for treating a disease associated with NF-kappaB activation, such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases, or ischaemic disorders.
                                                                                                                                                                                                                New purified protein that activates nuclear factor kappa B (NF-kappaB), useful for treating inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
                                                                                                                                                                                                                                                                                                                                                                    03-DEC-2001; 2001JP-00368692.
05-DEC-2001; 2001US-0335829P.
03-OCT-2002; 2002JP-00291302.
04-OCT-2002; 2002US-0415769P.
                                                    Sequence
                                                                                                                                                                             Claim
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DB; ADC37327.
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                                                     TACCAGGGCCCCTGCACCTTCCAGCTTCGGGACCCCGAGCAGCAGCAGCTGGAACTGAACCGG
                                                                                                CAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCCACCC
                                                                                                                          GTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; hlzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding a human TANGO 261 polypeptide.
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Claim, 2; Fig 5; 175pp; English
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                                                                                      Novel human and murine 266 and 267 useful as m
                                                                                                                                                               WPI; 2000-579269/54.
P-PSDB; AAB18449.
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                                                              treating cancer.
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                                                                                   secreted proteins designated TANGO 216, modulating agents of cellular processes,
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                  GGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTC
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Email: segref@genoscope.cns.tr, Web: www.genoscope.cns.tr  1st strand cDNA was primed with a NotI-oligo(dT) primer Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPRT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9945.r  9945.r  9945.r  11005  1.	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE	1 (bases 1 to 1005) Li,W.B., Gruber,C., Jessee, J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) On Feb 16, 2001 this sequence version replaced gi:31316780. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE	HSGY.  HOMO Sapiens (human)  Homo sapiens  Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  Hominidae; Homo.  1 (bases 1 to 1005)  1.i, W.B., Gruber, C., Jessee, J. and Polayes, D.  Full-length cDNA libraries and normalization  Unpublished (2001)  On Feb 16, 2001 this sequence version replaced gi:31316780.  Contact: Genoscope  Genoscope - Centre National de Sequencage  2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

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Pred. No. 1.2e-169;
B; Mismatches 10;
                                         sapiens cDNA clone
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                    CAGCGGGAC
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This sequence belongs to sequence cluster 9945.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODA008CA12NP1&c=9945.r.Location/Qualifiers
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr
Email: seqref@genoscope cros.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
1st strand cDNA was primed with a NotI of and cloned
1end enriched, double-strand cDNA was digested with Not I and cloned
1into the Not I and EcoRV sites of the pcMVSPORT 6 vector. Library
1 was not normalized. Library was constructed by Life Technologies, a
1 division of Invitrogen.
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1 (bases 1 to 1038)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 13, 2001 this sequence version replaced

Contact: Genoscope
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CTGCCACCCACCTTCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGC
                                           CTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTACCACCCTGC
                                                                                                                                                  CAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGAC
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/clone_lib="Homo sapiens NEUROBLASTOMA"
/clone="Vector: pc(MVSPORT 6; lst strand cDNA was primed
/note="Vector: pc(MVSPORT 6; lst strand cDNA was primed
double-strand cDNA was digested with Not I and cloned i
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 1e-168;
4; Mismatches
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                                                                                                                                                                                                       CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2493 row: g column: 18
High quality sequence stop: 571.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ641849 967 bp
AGENCOURT 8287174 NIH MGC 43 Homo
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ641849.1 GI:21766021
EST.
                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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1 (bases 1 to 967)
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/clone="IMAGE:629265"
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/clone=10rgan: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
/cloned into EcoRI/XhoI sites using the following 5'
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG (G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
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/db_xref="taxon:9606"
                                                                                                                                                                   organism="Homo sapiens"
/mol_type="mRNA"
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Matches 746; Conserv
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AGENCOURT_6707077 NIH_MGC_115
5', mRNA sequence.
BM922276
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
                                              Homo sapiens (human)
                                                                                         BM922276.1
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GI:19372655

ģ Homo

mRNA linear EST 12-MAR-2002 sapiens cDNA clone IMAGE:5754437

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SOURCE

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CAGGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGC
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GAGAAGGATAAACAGAAAGGACACCCTCTC
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Location/Qualifiers
1. .1046
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/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: hot1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5754437"
/lab_host="DH10B"
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Pred. No. 8.2e-145;
0; Mismatches 32;
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                                                                                                                                      693;
\vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae, Homo.

1 (bases 1 to 901)

Li,W.B., Gruber,C., Jessee,
Full-length cDNA libraries
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http://fulllength.invitrogen.com/ InVitroGen Corporat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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BU539219
BU539219.1 GI:22849660
EST.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC lone distribution: MGC proceedings of the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM7757 row: p column: 18
High quality sequence stop: 663.
                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                           CAGTGGGCCCCT-CCTTGCTGGAGGGGACCCGGCTCCACCACACACACACACTCGCG-CCC
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/tlosue_type="adenocarcinoma, cell line"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 107"
/clone lib="NIH MGC 107"
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/note="Organ: breast; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: breast; Vector: pOTB7; Site_1: EcoRI;
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pirectionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segraf@genoscope.cns.fr Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORW Homo sapiens con CSODJ015YF12 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODJ015DC06NP1&c=9945.r.Location/Qualifiers
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                                                                                                        AGCCAGGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAG
                                                                                                                                                                        AGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCCGCCTCGGCCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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/clone="CSDJ015YF12"
/cell type="T CELLS (JURKAT CELL LINE)
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mol_type="mRNA"
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Pred. No. 9.3e-142;
1; Mismatches 4;
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                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM13626 row: c column: 10
High quality sequence stop: 669.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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EST.
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AGENCOURT 8825282 Lupski_sciatic_nerve
IMAGE:6204609 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/clone lib="Lupski sciatic_nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGGGTCCG-3' and
                                                                                        /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                clone="IMAGE: 6204609"
                                                                                                                                               sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
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CDNA clone
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5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected

Matches 731; Query Match

61 70

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Local Similarity
BX362396 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED Homo sapiens cDNA clone CSODJO14YN15 3-PRIME, mRNA sequence.

BX362396 Homo sapiens cDNA clone CSODJO14YN15 3-PRIME, mRNA sequence.

BX362396 CGI:46307643

EST.

Homo sapiens (human)
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No. 1.4e-137;
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AUTHORS
TITLE
JOURNAL
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Best Local Similarity
Matches 683; Conserv
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr Web: www.genoscope.cns.fr
Email: segref@genoscope.cns.fr Neb: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae; Homo.

1 (bases 1 to 867)

Li.W.B. Gruber(C. Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)

On May 5, 2003 this sequence version replaced Contact: Genoscope
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODJ014CG08NP1&c=9945.r.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                      CGCCCGCTTCGGCCCACCGACCGCTTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTT
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                                                                                                                            GGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAAC
                                                                                                                                                                                                                                                                        CCACCGCTTCCAGCCCACCTATCCGTACNTGNAGNAGAGATNGACNTGCCGCCCACCAT
                                                                                                                                                                                                                                                                                               CCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCACCAT
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/mol_type="ndNA"
/db_xref="taxon:9606"
/clone="CSODJO14YM15"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.5%;
95.9%;
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Pred.
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No. 1.7e-137;
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ACCESSION VERSION KEYWORDS SOURCE

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AUTHORS
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2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: segref@genoscope.cns.fr
BM strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31283015.
Contact: Genoscope
Contact: Genoscope
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Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODJO15DC06QP1&c=9945.r. Location/Qualifiers
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                                                                                              GTGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCAC
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                                                                                                                                                                                                                                                                                                              /clone="CSODJ015YF12"
/cell type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED'
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"
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                                                                                                                                                          77.4%;
                                                                                                                                      Score 666.6; DB 1;
Pred. No. 2.1e-137;
2; Mismatches 1;
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                                                                             CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MCC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.lnl.gov
                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
                                                                                                                                                                                                                                                     Hominidae; Homo.

1 (bases 1 to 850)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian

Unpublished (1999)
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AGENCOURT 10016502 NIH MGC 142 Homo
IMAGE:6497853 5', mRNA sequence.
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Mammalia; Eutheria;
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                         quality sequence stop: 499.
Location/Qualifiers
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                                  CAGTGGGCCG-CCCTCCTTGCTGG-AGGGGACCCGGCTCCACCACACACACACACTCGCGCCC
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                GCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGG
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/db_xref="taxon:9606"
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97.9%;
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0; Mismatches
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PUBMED
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Best Local Similarity
Matches 648; Conserv
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, D., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rockville, MD 20850, USA These sequences were made them based on alignment.
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                                                                                                               Conservative
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/locus_tag="HCM6856"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 2.8e-133;
0; Mismatches 104;
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VIRTUAL TRANSCRIPT, partial sequence,
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West Gude Drive

Kejariwal, A.,

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Matches Query Match

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                                                                                                                                                                                                                                                                                        1 (bases 1 to 647)
Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.
Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
Zhang,X., Jay,G. and He,W.
High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DN992322 647 bp mRNA linear EST 17-MAY-2005 TC124411 Human adult whole brain, large insert, pCMV expression library Homo sapiens cDNA clone TC124411 5' similar to Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 4, mRNA sequence.
                                        http://www.origene.com
Seq primer: pCMV6 5prime
Technologies Inc.
                                                                                   OriGene Technologies, Inc.
6 Taft Ct. Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
                                                                                                                                             This EST submission is part of an on-going human full-length cloning project at OriGene Technologies, Inc. please contact OriGene for access.
                                                                                                                                                                                      Contact: Kovacs, KF
High Throughput cDNA Cloning
OriGene Technologies, Inc. ( www.origene.com )
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
Email: cDNA@origene.com
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/organism="Homo sapiens"
                         Location/Qualifiers
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                                                         vector
                                                         primer,
                                                         OriGene
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                                                                        DEFINITION
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Homo sapiens BQ636742
BQ636742.1 GEST.
Homo sapiens

GI:21761201

sapiens (human)

BQ636742 hd13h06.y1 Human Retina "---- Mapiens cDNA clone

609 bp cDNA (Un hd13h06

bp mRNA linear EST 15-(Un-normalized, unamplified): 106 5', mRNA sequence.

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ORIGIN
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                      GCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCG
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GCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCG
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                                                                        TGCGCGCACCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: Brain; Vector: pCMV6-XL5; Site 1: EcoR1; Site 2: Xhol/Sall compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and strict mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Whole brain"
/clone_Tib="Human adult whole brain, large insert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
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99.8%;
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Email: graeme@helix.nih.gov
Plate: 13 row: h column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), 196-204 (2002)
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  GCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGA 578
                                                                                   AGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGA
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unamplified): hd/he"
/note="Organ: Eye; Vector: psPORT1; Neural retina tissue
/note="Organ: Eye; Vector: psPORT1; Neural retina tissue
/mote="Organ: Eye; Vector: psPORT1; Neural retina tissue
/note="Organ: Eye; Vector: psPORT1; Neural retina to observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pspORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
Instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
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/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hd13h06"
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                                                                        Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                       Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komo,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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HTC; CAP trapper.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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The RIKEN Genome Exploration Research Group Phase
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Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

The FANTOM Consortium and the

RIKEN Genome Exploration Research

& II Team

Nature 409,

Functional annotation of a FANTOM Consortium.

685-690

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Best Local Similarity
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Pax:81-45-503-9216)

Please visit our web site (http://genome.gsc.riken.jp/) for further
                                                         GCACGTGCAACTG-CAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTT 123
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Search completed: February 28, 2006, 12:21:53 Job time: 3986.56 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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### SUMMARIES

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US-09-902-540-1002	US-09-902-540-868	US-09-902-540-3802	US-08-924-440-1	US-09-902-540-8322	US-10-148-806-3	US-09-724-797-15	US-09-775-398-42	US-09-476-242-3	US-08-485-246A-7	US-08-127-721A-7	US-08-476-176B-7	US-09-252-991A-7920	US-09-252-991A-7780	US-09-949-016-17361	US-09-949-016-12147	US-09-252-991A-660	US-09-252-991A-719	US-09-252-991A-692	US-08-785-420-1	US-09-252-991A-4200
Sequence 1002,	Sequence	sequence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
1002, Ap	44, App	-	I, Appii		J, Appii	15, App1	42, App1	3, Appli	7, Appli	7, Appli	7, Appli	7920, Ap	7780, AD		12147, A	660, App	•	692, ADD	F	4200, AD

# ALIGNMENTS

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Sequence 1, Application US/09769482

Patent No. 6566130

GENERAL INFORMATION:
APPLICANT: SRIVASTAVA, SHIV
APPLICANT: WOUL, JUDD W.
APPLICANT: WOUL, JUDD W.
APPLICANT: SEGAWA, TAKEHIKO
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION NUMBER: US/09/769,482
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,772
PRIOR APPLICATION NUMBER: 60/178,772
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.1
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US-09-769-482-1
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                                                                                                                                                                                                                                                                                                                                          Query Match 87.5%;
Best Local Similarity 99.5%;
Matches 756; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (95)..(850)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
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282 CTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCG
                                                                        211
                                                                                                         222 CCGGCACAGCCAGGGGGGGGAGGAGAGATGCCCCTGTCCTCAGAAGGATGCCTGTGGCC
                                                                                                                                                             151 GGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAG
                                                                                                                                                                                                       162 GGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAG
                                                                                                                                                                                                                                                                           102 GGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGAT 161
                                                                                                                                                                                                                                                    91 GGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGAT
                                                                        CCGGCACAGCCAGGGGGGGGGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCC
                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                          Score 753.6; DB 3;
Pred. No. 5.6e-158;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                       Length 1140;
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APPLICANT: SRIVASTAVA, SHIV
APPLICANT: WOUL, JUDD W.
APPLICANT: XU, LINDA L.
APPLICANT: SEGAWA, TAKEHIKO
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
FILE REFERENCE: 04995.0057-0000
CURRENT APPLICATION NUMBER: US/09/769,482
CURRENT PILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,772
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR FILING DATE: 2000-01-31
NUMBER: OF SEQ ID NOS: 67
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 759
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US-09-769-482-2
; Sequence 2, Application US/09769482
; Patent No. 6566130
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                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo
US-09-769-482-2
                                                                      Query Match
Best Local Similarity
Matches 754; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            571
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               1 ATGGCGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTG
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                                                                        87.4%; ilarity 99.7%; Conservative
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                                                                      Score 752.8; DB 3; Pred. No. 7.7e-158; 0; Mismatches 2;
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                                                                                                       Length
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                                                                                                                                                                                                                                                                          RESULT 3
US-09-091-952A-7
; Sequence 7, Application
; Patent No. 6458532
; GENERAL INFORMATION:
; APPLICANT: Detera
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NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            661
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                                                                                                                                                                                                                                                                                                                      Application US/09091952A
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                                                                                                                                  Badner, Judith A.
Badner, Judith A.
Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Esterling, Lisa E.
INVENTION: Chromosomal Markers and Diagnostic
"Marts for Manic-Depressive Illness
                                                                                                                                                                                                                                                        Detera-Wadleigh,
Gershon, Elliot
                                                                                                                                                                                                                                                                              Sevilla
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660 765 600 705 540 645 480 585 420 360

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LOCATION: 1...921
OTHER INFORMATION: Clone 22 coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-091-952A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 482;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 7:
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FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214
                                                                                                                                                                                                                                                                                                                      400
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                          574
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                                                                                                                                                                                           454
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                                                                                                                                                                                                                                                                            394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 ACGGTGATGGTGGTCATCGTCTGCCTGCTGAACCACTACAAAGTCTCCACGCGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 CCGGGCATCTTCAACTCGGAGCTGGAGTTCGCCCAAATCATCATCATCGTCGTGGTGGTC
                                                                  580
                                                                                                         514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 CAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatik
OPERATING SYSTEM: DOS
TTCGACAGTGACCTGATGGATAGTGCCAGG---CTGGGCGGCCCCTGCCCCCCCAGCAGT 630
                                                                                                                                                                                                                                                                                                                    TTCATCAGCCGGCACAGCCAGGGGGGGGGGGAGAAGATGCCCTGTCCTCAGAAGGATGC 273
                                                                                                                                                                                                                                                                     CTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCCAGAGCCGCAGGTCTACGCC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCATCAACCGCCCGAACCAGAGCCGGAGGCGGGAGGACGGGCTGCCGCAGGAAGGGTGC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/091,952A
                                                                                            CCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATC 573
                                                                                                                                                 CTGTCCGACGGTGAAGAGCCACCTCCTTACCAGGGGCCCTGCACCCTGCAGCTCCGGGAC 579
                                                                                                                                                                                             CTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGAC 513
                                                                                                                                                                                                                                    CGCTTCCAGCCCACCTACCCCTATGTGCAGCACGAGATTGATCTTCCTCCCACCATCTCC 519
                                                                                                                                                                                                                                                                                                                                                                                                         CTGTGGCCTTCAGACAGCGCCGCACCGCGGCTGGG-----CGCCTCGGAGATCATGCAT 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300
                                                               Conservative
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RESULT 4
US-091-952A-6
; Sequence 6, Application US/09091952A
; Patent No. 6458532
; GENERAL INFORMATION:
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COMPUTER: IBM COMPATIBLE
COPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: CUNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NUMBER: CT-1997
                                                                                                                                                                                                                                                                                                                    NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TITLE OF INVENTION: Chromosomal Markers and Diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Detera-Wadleigh, Sevilla D. Gershon, Elliot S.
                  FEATURE:
                                                                                                                                                                            TOPOLOGY: line MOLECULE TYPE: DNA
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                                                                                        FEATURE
                                                                                                                                                               FEATURE:
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                                                   NAME/KEY:
                                                                                                                          NAME/KEY:
LOCATION:
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CITY: San Francisco
                                                                                                       LOCATION: 1...806
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                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                      TELEX: <Unknown>
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                  LENGTH: 8065 base pairs
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Yoshikawa, Takeo
Sanders, Alan R.
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         CDS 116...1036 116...1036 coding region
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Sequence 65, Application US/09311021

Patent NO. 6706869

GENERAL INFORMATION:

APPLICANT: Wong, Gordon G.

APPLICANT: Fechtel, Kim

APPLICANT: Fechtel, Kim

APPLICANT: Genetics Institute, Inc.

APPLICANT: Genetics Institute, Inc.

TITLE OF INVENTION: SECRETED PROTEINS AND PORTICE GIOSO-11A

CURRENT APPLICATION NUMBER: US/09/311,021

CURRENT FILING DATE: 1999-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; IOCATION: 452...505
; OTHER INFORMATION: alternativ
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5595...5685
; OTHER INFORMATION: amplified
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-091-952A-6
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US-09-311-021-65
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Best Local
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NUMBER JOF
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SEQ J.D NOS: 268
                                                                                                                                                                                                                                                                                                                                       CCCGAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 452...50: OTHER INFORMATION:
                                                                                                                                                                                                    ACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                 CTGTCAGACGGGGAGGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGAC
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                                                                                                                                                                                                                                                         AACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGCGGCGCATGGAGGGGCCGCCGCCC
                                                                                                                                                                                                                                                                                                     TTCGACAGTGACCTGATGGATAGTGCCAGG---CTGGGCGGCCCCTGCCCCCCCAGCAGT
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                                                                                                                                                                                                                                                                                 Conservative
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                                              POLYNUCLEOTIDES
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; SOFTWARE: Patentl; SEQ ID NO 65; LENGTH: 937; LENGTH: 937; TYPE: DNA; ORGANISM: Homo 6US-09-311-021-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGAGCATGGAGATCACGGAGCTGGAGTTTTGTTCAGATCATCATCATCATCGTGGTGGTGAT 152
                    CACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCACCAGCAGAGCAG
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                                                                                           CTTCGACAGTGACCTGATGGATAGTGCCAGG----CTGGGCGGCCCCCTGCCCCCCCAGCAG
                                                                                                                                                                                                                                 CCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCAT
                                                                                                                                                                                                                                                                                                      GCTGTCAGACGGGGAGGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGA
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                                                                                                                                         CCTGTCCGACGGTGAAGAGCCACCTCCTTACCAGGGGCCCTGCACCCTGCAGCTCCGGGA
                                                                                                                                                                                                                                                                                                                                                        CCGCTTCCAGCCCACCTACCCCTATGTGCAGCACGAGATTGATCTTCCTCCCACCATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTGTGGCCTTCAGACAGCGCCGCACCGCGCTGGGG-----CGCCTCGGAGATCATGCA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTCATCAGCCGGCACAGCCAGGGGGGGGGGGGGGGAGAAGATGCCCTGTCCTCAGAAGGATG
cacatacagegaageteatecaceacecagececetertreetecareaceagegeag
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Pred. No. 8.5e-69;
0; Mismatches 169;
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US-09-091-952A-8

Sequence 8, Application US/09091952A

Patent No. 6458532

Patent No. 6458532

Patent No. 6458532

Patent No. 6458532

REPLICANT: Detera-Wadleigh, Sevilla D.
Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Esterling, Lisa E.
TITLE OF INVENTION: Chromosomal Markers and Diagnostic
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:

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OTHER INFORMATION: Clone 22 i

spliced coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-091-952A-8
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
AFTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REGISTRATION NUMBER: 015280-297100US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
TELEPAR: ATALERANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                        330
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                                                                                                                                                                                                                                                                                                                                                                                                                              166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 CAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCATCGTGGTGGTGATG 153
                                                                                                                                                                                                                                                                                                                                                                                                                              CCGGGCATCTTCAACTCGGAGCTGGAGTTCGCCCAAATCATCATCATCGTCGTGGTGGTC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGAC 513
                                                                                                                                 GCCCCGCGGTCCAGGGACAGGTTCACAGCGCCCGTCCTTCATCCAGAGGGATCGCTTCAGC: 405
                                                                                                                                                                                                                                             CTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCC 333
                                                                                                                                                                                                                                                                                                                  TTCATCAGCCGGCACAGCCAGGGGGGGGGGGGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGC 273
                                                                                                                                                                                                                                                                                                                                                     ACGGTGATGGTGGTCATCGTCTGCCTGAACCACTACAAAGTCTCCACGCGGTCC
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COUNTRY: USA
                                                                                                                                                                   CCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCAC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
                                                         CGCTTCCAGCCCACCTACCCCTATGTGCAGCACGAGATTGATCTTCCTCCCACCATCTCC 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KBY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
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Pred. No. 7.5e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone 22 isoform
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                                                                                                                                                                                                        -----GCCGCAGATCATGCAT 345
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NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2162
LENGTH: 391
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 17..223
US-09-621-976-2162
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US-09-621-976-2162
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Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 00/217,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dumas milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2162, Application US/09621976 Patent No. 6639063
                                                                                                                                                                               Sequence 6620, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                       607 GGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGC 666
                                                                                                                                                                                                                                                                                               146 TCTTTCCTCCATCACCAGCGCAGAACGC 173
                                                                                                                                                                                                                                                                                                                               727 TCCTTCCAGCACCAGCAGCAGCAGTGGGC
                                                                                                                                                                                                                                                                                                                                                                                              667 GGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCC
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Pred. No. 6.3e-11;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                   754
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APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

ITILE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT APPLICATION NUMBER: 60/217,883

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

INUMBER OF SEQ ID NOS: 16825

SEQ ID NO 506

LENGTH: 2364

TYPE: DNA

ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; PRIOR FILING DATE: 2000-07-10; NUMBER OF SEQ ID NOS: 16825; SEQ ID NO 6620; LENGTH: 645; TYPE: DNA; ORGANISM: Myxococcus xanthus US-09-902-540-6620
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US-09-902-540-506
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llarity 45.7%;
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Pred. No. 0.0016;
0; Mismatches 238;
                                             Score 57.2; DB 3;
Pred. No. 0.0022;
0; Mismatches 238;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiesand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Seq:
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
VUMBER OF SEQ ID NOS: 16825
SEQ ID NO 904
LENGTH: 11382
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-904
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US-09-902-540-904
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Best Local Similarity
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GTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCC 473
                                                                                                             CCTGGCCGTGCCGCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCC
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Pred. No. 0.024;
0; Mismatches 278;
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RESULT 11

US-09-902-540-8567, Application US/09902540

; Sequence 8567, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 8567

; LENGTH: 1884

TYPE: DNA
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Best Local Similarity 48.0%;
Matches 213; Conservative
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CCCGCATCAGGAGCAGCCACGCCCCACGACGCCACGACTGCCTTGGGTCCTGCTTCAGGC 1631
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                                                                                       CTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAA 632
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 52.6; DB 3; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1884;
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RESULT 13

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APPLICANT: HELLX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION UNMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
PRIOR FILING DATE:
1 NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1064
LENGTH: 2183
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-104-047-1064
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Patent No. 6943241
GENERAL INFORMATION:
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Best Local Similarity 46.8%;
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1073 CCCCA 1077
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                                  790 ACACA 794
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US-09-252-991A-13687
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; Patent No. 6551795
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PRILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Simil
Matches 179; (
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LENGTH: 1122
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GENERAL INFORMATION:
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              APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27.
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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NUMBER JE
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SEQ TO NOS:
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Pred. No. 0.066;
0; Mismatches 193;
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13650
LENGTH: 1452
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Search completed: February 28, Job time : 176.41 secs
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Pseudomonas aeruginosa
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Local Similarity 57.2%;
les 87; Conservative
                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                         AGCCAGGGGCGAGGAGAGAAGATGCCCTGTC 260
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                                                                        CGCCATCGCGAGGGGGGGATAGCCGCCCTGGC
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Pred. No. 0.18;
0; Mismatches 6
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1: /cgn2 6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2 6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*

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US-10-872-971-119

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US-10-287-436A-300

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US-11-51-454-412
US-10-241-220-44
US-10-872-972-44
US-10-872-991-4
US-09-821-812-2
US-09-821-812-2
US-10-49-635-2
US-10-390-045-1
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Sequence 15, App. Sequence 13116, A Sequence 20307, A	Sequence 197, App Sequence 16, Appl Sequence 1023, Ap Sequence 1023, Ap Sequence 1228, Ap Sequence 21, Appl	166	Sequence 45, Appl Sequence 45, Appl Sequence 71, Appl Sequence 12, Appl Sequence 32, Appl Sequence 57, Appl Sequence 14, Appl

## ALIGNMENTS

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APPLICANT: Lee, Richard T.

APPLICANT: Landschulz, Katherine T.

APPLICANT: Turi, Thomas G.

APPLICANT: Thompson, John F.

APPLICANT: Kennedy, Scott P.

APPLICANT: Kennedy, Scott P.

TITLE OF INVENTION: DIGNOSIS AND TREATMENT OF TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS

FILE REFERENCE: P0738/7001/ERP/KA
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Best Local Similarity 100.0%; Pred. No. 1.5e-219;
Matches 861; Conservative 0; Mismatches 0;
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LENGTH: 861
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTMARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo Sapiens FEATURE:
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LOCATION: (1)...(861)
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GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Afar, Natasha
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Hevezi, Peter
APPLICANT: Hevezi, Peter
APPLICANT: Mack, David H
APPLICANT: Marray, Richa
APPLICANT: Watson, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-10-295-027-127
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                APPLICANT: EOS Bictechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 0.8501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,366
PRIOR APPLICATION NUMBER: US 60/335,394
R APPLICATION NUMBER: US 09/663,733
R FILING DATE: 2000-09-15
APPLICATION NUMBER: US 60/350,666
FILING DATE: 2001-11-13
APPLICATION NUMBER: US 60/335,394
RELING DATE: 2001-11-15
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Gish, Kurt C.
Glynne, Richard
Hevezi, Peter A.
Mack, David H.
Murray, Richard
Watson, Susan R.
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PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 1386
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Local Similarity 100.0%;
hes 861; Conservative 0
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FILING DATE: 2001-11-21
APPLICATION NUMBER: US 60/334,393
FILING DATE: 2001-11-29
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                                                                                AGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGC
                                                                                                                                GAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCC
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Pred. No. 1.5e-219;
); Mismatches 0;

    See File Wrapper or PALM.

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APPLICANT: Turi, Thomas G.

APPLICANT: Thompson, John F.

APPLICANT: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA

CURRENT APPLICATION NUMBER: US/09/934,249

CURRENT FILING DATE: 2001-08-21

PRIOR FILING DATE: 2001-08-21

PRIOR PILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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TYPE: DNA
ORGANISM: Homo Sapiens
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LOCATION: (413)...(1273)
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GTGCCGCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTG
                                                                          AGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCA
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US-10-241-220-119
; Sequence 119, Application US/10241220
publication No. US20030148408A1
; GENERAL INFORMATION:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS .
TITLE OF INVENTION: TREATMENT OF TUMOR
TILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 119
                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 861; Conserv
                                                                                                                                                                                                                                                                           LENGTH: 4839
TYPE: DNA
ORGANISM: Homo
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APPLICANT: Hillan, Kenneth
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
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           TTTGTTCAGATCATCATCGTGGTGGTGGTGATGGTGATGGTGGTGATCACGTGC 180
                                              TCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG
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Spencer, Susan
Williams, P. Mickey
                                                                                                                                                                                  100.0%; Score 861; DB 6; Length ilarity 100.0%; Pred. No. 1.9e-219; Conservative 0; Mismatches 0; Indels
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Sequence 84, Application US/10269909

Publication No. US20030180747A1

GENERAL INFORMATION:

APPLICANT: HRUBAN, RALPH H.

APPLICANT: ARGANI PEDRAM

APPLICANT: IACOBUZIO-DONAHUE, CHRISTINE

APPLICANT: MAITRA, ANIRBAN

TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THE

FILE REFERENCE: 58303 (71599)

CURRENT APPLICATION NUMBER: US/10/269,909

CURRENT FILING DATE: 2003-10-11

PRIOR APPLICATION NUMBER: 60/328,609

PRIOR APPLICATION NUMBER: 60/328,754

PRIOR APPLICATION NUMBER: 60/332,754

PRIOR APPLICATION NUMBER: 60/332,754

PRIOR APPLICATION NUMBER: 60/332,754

PRIOR FILING DATE: 2001-11-19

NUMBER OF SEQ ID NOS: 87

SOFTWARE: PATEENTIN Ver. 2.1

SEQ ID NO.84

LENGTHA; 4889
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US-10-269-909-84
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US-10-269-909-85

; Sequence 85, Application US/10269909

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APPLICANT: HRUBAN, RALPH H.

APPLICANT: ARGANI, PEDRAM

APPLICANT: ACOBUZIO-DONAHUB, CHRISTINE

APPLICANT: MAITRA, ANIRBAN

TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES

FILE REFERENCE: 58303 (7169)

CURRENT APPLICATION NUMBER: US/10/269,909

CURRENT FILING DATE: 2003-10-11

PRIOR APPLICATION NUMBER: 60/328,609

PRIOR FILING DATE: 2001-10-11

PRIOR APPLICATION NUMBER: 60/332,754

PRIOR APPLICATION NUMBER: 60/332,754

PRIOR FILING DATE: 2001-11-19

NUMBER OF SEG ID NOS: 87

SOFTWARE: Patentin Ver. 2.1

SEG ID NO 85

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; TYPE: DNA
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Pred. No. 1.9e-219;
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; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-872-972-119
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US-10-872-972-119
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APPLICANT: Hillan, Kenneth
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Micke
APPLICANT: Wi, Thomas
APPLICANT: Wannes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/872,972
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/10/241,220
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; S
Best Local Similarity 100.0%; F
Matches 861; Conservative 0;
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
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CAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCCACCC
                               GTGCCGCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTG
                                                 GTGCCGCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTG
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Williams, P.Mickey
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Pred. No. 1.9e-219;
0; Mismatches 0;
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF TUMOR
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/872,991
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/10/241,220
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOMBER: US/10/241,220
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 119
LENGTH: 4839
TYPE: DNA
ORGANISM: Homo Sapien
US-10-872-991-119
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US-10-872-991-119
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Best Local Similarity
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                                                                                                                                                                                Matches
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APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
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Williams, P.Mickey
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                                                                                                                                                                                                            Length 4839;
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                                                                                           RESULT 9
US-10-287-436A-300
US-10-287-436A-300
; Sequence 300, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL IMFORMATION:
APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TRE.
TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872-514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 300
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                                 US-10-287-436A-300
    Query Match
                                                LENGTH: 4839
TYPE: DNA
ORGANISM: Homo sapiens
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RESULT 10
US-09-796-753-55
                                                                                        Sequence 55, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
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APPLICANT: MCCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND
FILE REFERENCE: 7853-27-999
CURRENT APPLICATION NUMBER: US/09/796,753
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PRIOR APPLICATION NUMBER: 09/183,175

PRIOR FILING DATE: 1998-10-30

PRIOR APPLICATION NUMBER: 09/223,094

PRIOR FILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/224,246

PRIOR APPLICATION NUMBER: 09/224,246

PRIOR APPLICATION NUMBER: 09/259,388

PRIOR APPLICATION NUMBER: 09/259,388

PRIOR APPLICATION NUMBER: 09/259,388

PRIOR APPLICATION NUMBER: 09/259,388

PRIOR APPLICATION NUMBER: 09/312,458

PRIOR APPLICATION NUMBER: 09/312,458

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: 09/312,359

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: 09/312,359

PRIOR FILING DATE: 1999-03-01
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PRIOR PILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/34/
PRIOR APPLICATION NUMBER: 09/34/
PRIOR APPLICATION NUMBER: 09/34/
PRIOR FILING DATE: 1999-06-39
PRIOR APPLICATION NUMBER: 09/36/
PRIOR APPLICATION NUMBER: 09/36/
PRIOR APPLICATION NUMBER: 09/36/
PRIOR APPLICATION NUMBER: 09/39/
PRIOR APPLICATION NUMBER: 09/40/
PRIOR APPLICATION NUMBER: 09/47/
PRIOR APPLICATION NUMBER: 09/47/
PRIOR FILING DATE: 1999-12-23/
PRIOR APPLICATION NUMBER: 09/47/
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PRIOR APPLICATION NUMBER: 09/47/
PRIOR APPLICATION NUMBER: 09/51/
PR
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LENGTH: 969
TYPE: DNA
ORGANISM: Homo se
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PRIOR APPLICATION NUMBER: 09//
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09//
PRIOR FILING DATE: 2000-06-22
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FILING DATE: 2000-06-29
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Pred. No. 2.5e-191;
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RESULT 11
US-10-205-823-412
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APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Ganavarapu, Manj
APPLICANT: Gorbatcheva, Bell
APPLICANT: Hoersch, Sebastia
APPLICANT: Kamatkar, Shubhan
APPLICANT: Wonney, Angela M.
APPLICANT: Glatt, Karen
                                                                                                                                                                                                                                                                                                                         Sequence 412, Application US/10205823 Publication No. US20030108963A1 GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DAGE: 2001-08-22
                                                                                             APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSI
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
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Kamatkar, Shubhangi
Wonsey, Angela M.
Glatt, Karen
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Endege, Wilson O.
Gannavarapu, Manjula
Gorbatcheva, Bella
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US-10-301-822-208
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PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
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Best Local S
Matches 762
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                                                                                                AGAGAGCGCAGCCATCTGGAGCAAAGAAGGATAAACAGAAAGGACACCCTCTC 861
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                                                                  AGAGAGCGCAGCCATCTGGAGCAAAGAAGGATAAACAGAAAGGACACCCTCTC
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98.3%;
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Pred. No. 4.8e-191;
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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEC ID NOS: 228
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NAME/KEY: CDS
LOCATION: (96)...(854)
JS-10-301-822-208
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 208
LENGTH: 1141
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Best Local Similarity
Matches 762; Conserv
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                                                                                                                                                      CATCTCGCTGTCAGACGGGAGGAGGACCCCACCCTACCAGGGCCCCTGCACCCTCCAGCT
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                  AACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAG
                                                                                                  TCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAG
                                                                                                                                                                                   CATCTCGCTGTCAGACGGGGAGGAGCCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCT
                                                                                                                                                                                                                                                                                                              CTACGCCCGCCTCGGCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCG
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AACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCCAG
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98.3%; Pred. No. 4.8e-191;
rative 0; Mismatches 13;
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APPLICANT: ALIGO, AND
APPLICANT: ADDETION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT PAPLICATION NUMBER: US/11/051,454
CURRENT FILING DATE: 2005-02-04
PRIOR APPLICATION NUMBER: US/11/205,823
PRIOR APPLICATION NUMBER: US/11/205,823
PRIOR FILING DATE: 2002-07-25
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-08-22
PRIOR RELING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR PILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR PILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR RELING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 412
LENGTH: 1141
TYPE: DNA
CREANISM: Homo sapiens
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US-11-051-454-412
; Sequence 412, Application US/11051454
; Publication No. US20050191673A1
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APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Wonsey, Angela M.
APPLICANT: Glatt, Karen
APPLICANT: Glatt, Karen
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Best Local S
Matches 762
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                                                                                                                                                                                                              Local Similarity
les 762; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gannavarapu, Manjula
Gorbatcheva, Bella
                                                                    GGTGATGATGGTGGTGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGC 206
                                                                                                                                                    TTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCATCGTGGT 146
  ACGGTCCTTCATCAGCCGGCACAGCCAGGGGGGGGGAGGAGAAGATGCCCTGTCCTCAGA 266
                                            GGTGATGATGGTGATGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGC
                                                                                                                                TCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT
                                                                                                                                                                                                                87.6%; ilarity 98.3%; Conservative
                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                Score 754.2; DB 10;
Pred. No. 4.8e-191;
0; Mismatches 13;
                                                                                                                                                                                                                                                             Length 1141;
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Sequence 44, Application US/10241220

Publication No. US20030148408A1

GENERAL INFORMATION:

APPLICANT: Frantz, Gretchen

APPLICANT: Hillan, Kenneth J.

APPLICANT: Phillips, Heidi

APPLICANT: Polakis, Paul

APPLICANT: Spencer, Susan

APPLICANT: Williams, P. Mickey

APPLICANT: Zhang, Zemin

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIA

TITLE OF INVENTION: TREATMENT OF TUMOR

FILE REFERENCE: P501081-US

CURRENT APPLICATION NUMBER: US/10/241,220

CURRENT FILING DATE: 2002-12-13

NUMBER OF SEQ ID NOS: 120

TEURIC NUMBER OF SEQ ID NOS: 120

TEURIC NUMBER OF SEQ ID NOS: 120
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                                                              ; TYPE: DNA
; ORGANISM: Homo
US-10-241-220-44
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US-10-241-220-44
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 Query Match
Best Local Similarity
Matches 762; Conserv
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Conservative
                                                                          Sapien
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                        87.6%;
98.3%;
              <u>.</u>
             Score 754.2; DB 6;
Pred. No. 5.1e-191;
0; Mismatches 13;
                                     Length 1850;
               Indels
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               Gaps
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                                                                                                GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Micke
APPLICANT: Wu, Thomas
                                                                                                                                                                                                     RESULT 15
US-10-872-972-44
; Sequence 44, Application US/10872972
; Publication No. US20040229277A1
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: TREAGMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/872,972
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/10/241,220
PRIOR FILING DATE: 2002-09-11
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; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 44
; LEGATH: 1850
; TYPE: DNA
; ORGANISM: Homo Sapien
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Search completed: February 28, 2006, 15:52:48 Job time: 812.676 secs

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Maximum DB seq length: 200000000
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                                                                                            Published Applications NA New:*

1: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

2: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

3: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

4: /cgn2 6/ptodata/2/pubpna/PCT NEW PUB.seq:*

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10: /cgn2 6/ptodata/2/pubpna/US11 NEW PUB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
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1626.862 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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4.9	4.9	4.9	5.0	5.0	5.0	5.0	5.0	5.1	5.1	5.1	5.2	5.3	5.9	7.1	7.2	7.4	9.3	10.2	87.6	Query Match
2257	9729	8831	1088	7402	7402	2736	646	2226	78869	11070	200628	2561	2183	63	97	97	129	94	1141	Query Match Length
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US-10-770-726-16	US-10-412-748-10	US-10-412-748-12	US-09-925-065A-69151	US-10-750-623-27313	US-10-750-185-27313	US-10-858-730-38	US-09-925-065A-607564	US-11-052-554A-545	US-11-075-185-1	US-11-075-185-34		US-11-127-877-26	US-11-072-512-1064	US-10-310-914A-7162	US-10-310-914A-1107	US-10-310-914A-6542	US-10-310-914A-7163	US-10-310-914A-1106	US-11-186-284-208	ID
Sequence 16, Appl	Sequence 10, Appl	Sequence 12, Appl	Sequence 69151, A	Sequence 27313, A	Sequence 27313, A	Sequence 38, Appl	Sequence 607564,	Sequence 545, App	Sequence 1, Appli	Sequence 34, Appl	Sequence 62, Appl	Sequence 26, Appl	Sequence 1064, Ap	Sequence 7162, Ap	Sequence 1107, Ap	Sequence 6542, Ap	Sequence 7163, Ap	Sequence 1106, Ap	Sequence 208, App	Description

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4.6	6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.8	4.8	4.8	4.9
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US-11-136-527-336	US-09-925-065A-934808	US-11-121-086-22	US-11-136-527-2896	US-11-112-908-35	US-11-112-908-36	US-10-750-623-19533	US-10-750-185-19533	US-09-925-065A-408177	US-11-012-668-15	US-11-112-908-55	US-11-112-908-56	US-10-955-054A-71	US-11-136-527-3303	US-11-124-368A-15273	US-10-131-826A-9	US-11-136-527-2427	US-09-925-065A-119552	US-11-176-253-2	US-11-183-136-5	US-11-136-619-3	US-09-925-065A-71692	US-09-925-065A-213874	US-11-121-086-28	US-11-205-109-1
Sequence 336, App	Sequence 934808,	Sequence 22, Appi	Sequence 2896, Ap		Sequence 36, Appl	Sequence 19533, A	Sequence 19533, A	Sequence 408177,	Sequence 15, Appl	Sequence 55, Appl	Sequence 56, Appl	Sequence /1, Appl	Sequence 3303, Ap	Sequence 152/3, A	Sequence 9, Appri	Sequence 2427, Ap	Sequence 119552,	Sequence 2, Appli	sequence 5, Appri	sequence 3, Appri	sequence /1692, A	sequence 2138/4,	Sequence 28, Appr	Sequence 1, Appli

### ALIGNMENTS

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; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(854)
US-11-186-284-208
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                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR PILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Millennium Pharmaceuticals, Inc.
Query Match 87.6%;
Best Local Similarity 98.3%;
Matches 762; Conservative
                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 208
LENGTH: 1141
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APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: MCTHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
TILE REFERENCE: MPMOI-029P2RNM
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Guillemette, Tra
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     Score 754.2; DB 12;
Pred. No. 1.6e-168;
0; Mismatches 13;
                                                        DB 12;
          Indels
                                                     Length 1141;
          0; Gaps
            0,
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APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of:

TITLE OF INVENTION: Uses thereof

FILE REPERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1386402

SOFTWARE: Patentin version 3.3

SEQ ID NO 1106

LEMIGHT: 944

TYPE: RNA

ORGANISM: Human

US-10-310-914A-1106
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US-10-310-914A-1106/c
                                                                                                                                                                                                         Sequence 1106, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
Query Maťch
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   . 28;
   Score 87.6;
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RESULT 3
US-10-310-914A-7163/c
; Sequence 7163, Application US/10310914A
; Publication No. US20060003322A1
; Publication No. US20060003322A1
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                                                                                                      ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-6542
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; ORGANISM: Human
US-10-310-914A-7163
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1384402
SOFTWARE: Patentin version 3.3
SEQ ID NO 7163
                                               Query Match
Best Local Similarity
Matches 64; Conserv
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Best Local
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CGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAAGGACACCC
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Pred. No. 9.3e-10;
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US-10-310-914A-1107/c
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US-10-310-914A-7162/c
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RESULT 7
US-11-072-512-1064
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LENGTH: 97
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SEQ ID NO 7162
LENGTH: 63
TYPE: RNA
ORGANISM: Human
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Best Local S
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 1082-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-11-06
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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ORGANISM: Human
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nes 62; Conservative
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98.4%;
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Pred. No. 2.1e-05;
0; Mismatches 1;
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Pred. No. 1.3e-05;
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; ORGANISM: Homo
US-11-072-512-1064
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APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: 084335-0191
FULB REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
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GENERAL INFORMATION:
APPLICANT: ISOGAI, TI
APPLICANT: SUGIYAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1064
LENGTH: 2183
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Best Local Similarity 46.8%;
Matches 227; Conservative
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NAGAI, KEIICHI
IRIE, RYOTARO
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YAMAMOTO, JUN-ICHI
ISONO, YUUKO
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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Pred. No. 0.0078;
D; Mismatches 25
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RESULT 9
US-11-121-086-62/c
US-11-121-086-62/c
Sequence 62, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: NIELSEN, TIM S.
APPLICANT: NULSEN, KIRSTEN V.
APPLICANT: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
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US-11-127-877-26/c
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; LENGTH: 2561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-26
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CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
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APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F.
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TITLE OF INVENTION: Methods, Compositions
TITLE OF INVENTION: Amyloid-Beta Protein
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SOFTWARE: PatentIn version 3.3
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Pred. No. 0.15;
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GENERAL INFORMATION:
APPLICANT: REBVES, CHRISTOPHER D
APPLICANT: REID, BRYAN
APPLICANT: REID, RALPH
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR
FILE REFERENCE: 010099.03
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR PILING DATE: 2004-05-04
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US-11-075-185-34
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SOFTWARE: PatentIn version
SEQ ID NO 62
LENGTH: 200628
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Publication No. US20050266434A1
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ORGANISM: Homo sapiens
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GCCTCGCCGACCGCGATGGCTACGTCCTCAGCGGCCGCCTCTCCACCAGCGACCACCCGT
                                                                                             GAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCA
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ilarity 43.9%;
Conservative
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Pred. No. 0.35;
0; Mismatches 243;
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Pred. No. 0.35;
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US-11-075-185-1
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CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.3
RESULT 12
US-11-052-554A-545/c
; Sequence 545, Appl
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LENGTH: 78869
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Best Local Similarity
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APPLICANT: JULIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FILE REFERENCE: 010099.03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Sorangium cellulosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11202 GCGCCGCCGGCGCAGAGTGCCTCGCTCCCGACGGCGTCGCGACGCCGGCTTCGTCCCCA
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                                                                                                                                                                                                                                                                                                                             GCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGCGCCATGGAGGGGCCCGC
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                                                                                      TGGCGTGGGCGGC 11634
                                                                                                                      TAGAGAGCGCAGC 818
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Application US/11052554A
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RESULT 13

US-09-925-065A-607564/c

Sequence 607564, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.

ITILE OF INVENTION: Identification and Mapping of Single
ITILE OF INVENTION: Nucleotide Polymorphisms in the Human G

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20
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APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

FILE REFERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: Patentin version 3.3
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Local Similarity 45.6%;
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Pred. No. 0.35;
0; Mismatches 230;
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APPLICANT: Walbridge, Michael J.
APPLICANT: Walbridge, Michael J.
APPLICANT: Worgey, Peter S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: 14184-030001
CURRENT APPLICATION NUMBER: US/10/858,730
CURRENT FILING DATE: 2004-06-01
PRIOR PILING DATE: 2004-06-01
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: US 60/475,000
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 364
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-858-730-38
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; ORGANISM: Homo sapiens
US-09-925-065A-607564
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 38
LENGTH: 2736
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LENGTH: 646
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APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-9
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PastSEQ for Windows Version 4.0
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APPLICANT: Blomquist, Paul
APPLICANT: Doten, Reed
APPLICANT: Driggers, Edward
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                                              333 CCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCA 392
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O'Toole, George
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APPLICANT: HOLM, Tom
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APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
CAPPLICANT: BATES, Stephen
APPLICANT: MILION-2
FILE REFERENCE: MMILION-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTMARE: Patentin version 3.1
SEQ ID NO 27313
LENGTH: 7402
TYPE: DNA
ORGANISM: BOVINE 19866880890824
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                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSEMFELD, David
APPLICANT: HOLM, Tom
                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                       1692 ATAGAGATGATGGTGGTGATAGTGGTGATGGTGGTGATGCTGGTGATGATGATGGTG
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<pre>/mol_type="unassigned /db_xref="taxon:9606"</pre>	rce	۲	Diagnosis and treatment of cardiovascular	AUTHORS Lee, R.T., Landschulz, K.T., Kennedy, S.P.,	Hominidae; Homo.	M Homo sapiens Eukaryota; Metazoa;	Homo sapiens	AX392417.1	Sequence 1 from Patent WO0216416.	117 AV302417 1321 hm DNA	i			28 2.1 2446 8 28 2.1 2446 8	498 28 2.1 2345 15 498 28 2.1 2345 15	496 28 2.1 2145 8	28 2.1 2145 6 28 2.1 2145 6	28 2.1 2145 6 28 2.1 2145 6	28 2.1 2145 6	489 28 2.1 2000 6	487 28 2.1 1915 15 488 28 2.1 1947 6	485 28 2.1 1/29 15 486 28 2.1 1834 15	484 28 2.1 1650 6	28 2.1 1334 15 28 2.1 1384 8	480 28 2.1 1300 15 481 28 2.1 1322 15	479 28 2.1 1203 6	28 2.1 1132 15 28 2.1 1203 6	28 2.1 1099 15	28   2.1   1094   15 $28   2.1   1094   15$	28 2.1 1094 15	28 2.1 933 5 28 2.1 1044 15	470 28 2.1 898 5	468 28 2.1 843 15 469 28 2.1 884 5	28 2.1 777 6	28 2.1 774 6 28 2.1 774 6	28 2.1 774 6	28 2.1 771 6	28 2.1 680 10 28 2.1 700 6	458 28 2.1 614 8 459 28 2.1 636 6	28 2.1 570 15 AK11101
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Patent: WO 2005064009-A 82 14-JUL-2005;
Aros Applied Biotechnology APS (DK)
Location/Qualifiers
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/db_xref="taxon:9606"
/note="transmembrane,
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Target genes for the diagnosis and treatment of cancer
Patent: WO 2004038020-A 109 06-WAY-2004;
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CQ896247 LOCUS DEFINITION Sequence 71 from Patent WO2004076614.  ACCESSION CQ896247 VERSION CQ896247 CQ896247.1 GI:55468096 KEYWORDS SOURCE ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  REFERENCE AUTHORS Hinzmann, B., Dahl, E., Rosenthal, A., Specht, T., Schmitt, A., Beckmann, G., Bruemmendorf, T., Kinneman, H., Xinzhong, L., Pilarsky, C. and Staub, E. Xinzhong, L., Pilarsky, C. and Staub, E. Human nucleic acid sequences obtained from prostatic carcinomas Patent: WO 2004076614A.  FEATURES FEATURES Specht, Thomas (DE); Schmitt, Armin (DE) FEATURES Source  1. 4839	Db 1141 TCTGGAGCAAAGAAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCC 1200.  Qy 1293 GGGCTGGGGTGGATAAACAGGAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCC 1200.  Qy 1291 GGGCTGGGGCTGAGATAGGCAG 1321		Db 841 AGCAGCTGAACTGAACCGGAGTCGGTGCGCCCAAACAGAACCATCTTCGACA 900  Qy 993 GTGACCTGATGGATAGTGCCAAGCTGGGCGCCCCTGCCCCCCAGCAGTAACTCGGGCA 1052	813 AGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCACCACCATCTCGCTGTCAG 8	Db 481 TGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCA 540  Qy 633 GCCGGCACAGCCAGGGGGCGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGC 692
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Oy  273 GACCCGAGCCCGGCGAGCCGGGGGCGCCTCCCCGCGCGCG	Query Match  93.0%; Score 1229; DB 6; Length 4839;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 93 GGAAAGCTAGCGCAGAGGCTCAGCCCCGGCGCAGCCCCATT 152  Db 1 GGAAAGCTAGCGGCAGAGGCTCAGCCCCGGCGCAGCCCCGCTGCCAGCCCATT 60  Qy 153 TTCCGGACGCCACCCGGGGGCACTGCCGAGGGCTGCCAAGGGGAAGGCCGGGG  Db 61 TTCCGGACGCCACCCGGGGCACTGCCGACGGCTGCCGAGGGGAAGCCCGGGG  Qy 213 GGGCGCAGCGCACCGGCGGCACTGCCGAGGCCCCGGGGAACTTGGCGGG 120  Db 121 GGGCGCAGCGGAGCGCGGCGCCCCCGCGGCACTGCCGAGGCCCGGGG 120  GGGCGCAGCGGAGCGCGGGCGCCCCCGCGCACTGAGCCCCCGGGAAACTTGGCGGC 272  Db 121 GGGCGCAGCGGAGCGCGCGCCCCCGCGCACTGAGCCCCCGGGGAACTTGGCGGC 272	ORGANISM Homo sapiens (numan)  ORGANISM Homo sapiens  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalla; Eutheria; Euarchontoglires; Primates; Catarrhini;  REPERENCE Hominidae; Homo.  AUTHORS Einstein,R., McGowan,K.M. and Pando,M.P.  TITLE Prostate specific genes and the use thereof as targets for prostate cancer therapy and diagnosis  JOURNAL Patent: WO 2004113571-A 166 29-DEC-2004;  Exonhit Therapeutics S.A. (FR)  FEATURES Exonhit Therapeutics S.A. (FR)  FOURMAL Patent: WO 2004113571-A 166 29-DEC-2004;  Exonhit Therapeutics S.A. (FR)  Location/Qualifiers  Source /organism="Homo sapiens" /mcl_type="unassigned DNA" /db_xref="taxon:9606"		Oy  1053 TCAGCGCCAACGTGCTACGGCAGCGGCGCCATGGAGGGGCCGCCCCTACAGCG 1112
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NF-kB activating gene
Patent: WO 03048202-A 159 12-JUN-2003;
Asahi Kasei Kabushiki Kaisha (JP)
Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/db_xref="taxon:9606"
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Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,		533 TTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGGTGGTGGTGGTGGTGATCACGTGC 592	, 9
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stanleton, M. Soares, M.B., Bonaldo, M.F., Casavant, T.L.,		473 TCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG 532	B &
Hominidae; Homo.  CE 1 (bases 1 to 1061)  Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,  Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M.	REFEREN AUTHO	413 ATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGCCGGCAGGCA	Qу
MSIN	SOURCE	Query Match 65.2%; Score 861; DB 6; Length 861; Best Local Similarity 100.0%; Pred. No. 0; Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Que Bes Mat
JT 11  Solution in the property of the propert	RESULT 1 BC015911 LOCUS DEFINITI ACCESSION KEYWORDI	/db_xref="GI:19700735 /translation="MHRLMGG IIIVVMMMVMVUTICLUSHY GIPEPQVYAPPRETDRLAVPE YGGPCTLOLRDPEQOLELNRR YGGGGRMEGPPFTYSEVIGHY KEKDKQKGHPL"	ORIGIN
1253 AAACAGAAAGGACACCCTCTC 1273 	D Qy	CDS 1>861- /note="unnamed protein product" /codon start=1 /protein id="CAD29006.1"	
1193 CTCCACCACACACACACGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAAGGAT 1252 	Qy	SOUTCE 1861  /organism="Homo sapiens" /mol type="unassigned DNA" //hb Tref-"nassigned DNA"	7 5 4 1
1133 GGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGG 1192	Qy Db	TITLE Diagnosis and treatment of cardiovascular conditions  JOURNAL Patent: WO 0216416-A 3 28-FEB-2002;  THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)	TII JOL
AGCGGCGGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACCTACCCG	da 43	REFERENCE 1 AUTHORS Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and	REFEH AUT
1013 AGGCTGGGCGCCCCCCCCCCCCAGGAGTAACTCGGGCATCAGCGCCACGTGCTACGGC 1072	Q dd Qy	NISM	SOURCE ORGA
953 GAGTCGGTGCGCCCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCC 1012	Qy Db	DEFINITION Sequence 3 from Patent WO0216416.  ACCESSION AX392419 VERSION AX392419.1 GI:19700734	DEFINIT ACCESSI VERSION
893 TACCAGGGCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGG 952	Qy Db	T 10	RESULT AX3924
833 CAGCACGAGATCGACCTGCCACCACCATCTCGCTGTCAGACGGGGAGGAGGCCCCCACCC 892	Qy Db	1313 AAAAGGCAG 1321           901 AAAAGGCAG 909	D QQ
773 GTGCGGCCCTTCGGCGAGCGGAGAGCGCTTCCACCGTTCCAGCCCACCTATCCGTACCTG 832	Qy Db	1253 AAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGGCTGGGGCTGGGGTAGGTG 1312	Db QQ
713 GGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCG	Qy Db	1193 CTCCACCACACACACCGCGCCCCTAGAGAGCGCAGCGATCTGGAGCAAAGAGAAGAGT 1252 	Db QQ
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593 CTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGGCG 652	Qy Db	1073 AGCGGCGGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCG 1132	g Q
121 TTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGC 180	Db	601 AGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGC 660	Ф

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PUBMED
REFERENCE
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAL Plate: 29 Row: e Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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Submitted (15-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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Tissue Procurement: DCTD/DTP
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         CTAGGGTCCCCAGGGGGCCGGGCTGGGGCTGCGTAGGTGAAAAGGCAG 1321
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCAT
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                                                                                                   GCAGGTCTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCG
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/note="BCAS2; Region: Breast carcinoma amplified sequence
/note="BCAS2; Region: Breast carcinoma amplified sequence
2 (BCAS2). This family consists of several eukaryotic
sequences of unknown function. The mammalian members of
this family are annotated as breast carcinoma amplified
sequence 2 (BCAS2) proteins. BCAS2 is a putative
spliceosome associated protein"
/db_xref="CDD:pfam05700"
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Pred. No. (
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                         GCCACTACCCGGGGTCCTCCCAGCACCAGCAGCAGTGGGCCGCCCTCCTTGCTGG 1181
                                                                            CGTGCTACGGCAGCGGCGCGCCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCG
                                                                                                        TGGATAGTGCCAGGCTGGGCGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-JAN-2000) CPDR, Rockville, MD 20852, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moul, J.W. and Srivastava, Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics 66 (3), 257-263 (2000)
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A novel androgen-regulated gene, PMER
20q13 exhibits high level expression
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1 (bases 1 to 1141)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xu,L.L., Shanmugam,N.,
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                                                                             induce="type 1b transmembrane protein; expression is induced in response to the synthetic androgen, R1881; expression is abundant in, and restricted to, prostate glandular epithelial cells; similar to the predicted protein encoded by sequence deposited at GenBank Accession Number Np 004329"
                                                                  SLLEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL"
                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                  gene="PMEPA1"
                                                                                                                                                                                                                                                                                                                             gene="PMEPA1"
                                                                                                                                                                                                                                                                                                                                                              /map="20q13.31-13.33"
/cell_line="LNCap"
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lva,S.
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1 (bases 1 to 1818)

Brunschwig, E.B., Wilson, K., Mack, D., Dawson, D., Lawrence, willson, J.K., Lu, S., Nosrati, A., Rerko, R.M., Swinler, S., Wilson, J.K., Lu, S., Willis, J., Platzer, P. and Markowitz, S. Lutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S.
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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SESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTYPYLQHEIDLPDTISL
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Patent: WO 2005064009-A 128 14-JUL-2005;
Paros Applied Biotechnology APS (DK)
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Mammalia; Eutheria;
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/note="transmembrane, pros
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                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/note="transmembrane, prostate
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Srivastava, S., Moul, J.W., Xu, L.L. and Segawa, T.
Androgen-regulated gene expressed in prostate tissue
Patent: US 6566130-A 2 20-MAY-2003;
Henry M. Jackson Foundation for the Advancement of M.
Medicine; Rockville, MD
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                                                                                                          Homo Bapiens (human)
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Bukaryota; Metazoa; Chordata; Craniata; Primates; Cata
Mammalla; Butheria; Buarchontoglires; Primates; Cata
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FRASER
PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68,
G01N33/15,
PC G01N33/50, G01N33/53, G01N33/53, G01N33/566, C12N15/00, C12N5/00
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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AX775887
AX775887.1
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Patent: WO 03048202-A 157 12-
Asahi Kasei Kabushiki Kaisha
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 1001
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/db_xref="GI:32693606"
/translat.on="waklepyOjilityvvmywvvvitcllshyklsarsfisrhsQG
rrredalssegclwpsestvsgngipepQvyappretdrlavpppaQrerfhreQpty
pyLQHEIDLPTISLSDGEEpppYQGPcTLQLDEDEQQLELNRESVRAppnrTiFDSD
LMDSARLGGPcPpSSNSGISATCYSGGEPPTYSEVIGHYPGSSFQHQQSSGPP
SLLEGTRLHHTHIAPLESAAIWSKEKDXQKGHPL"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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S Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.

S Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.

S Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.

S Ecreted proteins and nucleic acids encoding them

Patent: JP 2002539773-A 53 26-NOV-2002;

MILLENNIUM PHARMACEUTICALS INC

OS Homo sapiens (human)

PN JP 2002539773-A/53

PD 26-NOV-2002

PN JP 2002539773-A/53

PD 26-NOV-2002

PP 01-MAR-2000 JP 2000602247

PP 01-MAR-2000 JP 2000602247

PR 01-MAR-2009 US 60/122458

PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CH

PI FRASER

PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C

G01N33/15,

G01N33/50, G01N33/53, G01N33/53, G01N33/566, C12N15/00

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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JOURNAL
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  Hominidae; Homo.

The library homo sapiens (human)

PR 01-MAR-1999 US 60/122458

Hominidae; Homo.

Homo
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                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                   BD272514.1 GI:33082282 JP 2002539773-A/23.
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Secreted proteins and nucleic acids encoding them FH Key
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r CDS (6). (761).
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                                                                        AAGGATAAACAGAAAGGACACCCTCTCTAGGGGTCCCCAGGGGGGGCCGGGCTGGGGGCTGCG
                                                                                                                               ACCCGGCTCCACACACACACACCGCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAG
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                                                                                                                                                                                                                                                                                        AGTGCCAGGCTGGGCGCCCTGCCCCCCAGCAGTAACTCGGGGATCAGCGCCACGTGC 1066
                                                                                                                                                                                                                                                                                                                                  AACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGAT
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Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BD272545
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Best Local Similarity
Matches 754; Conserv
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Homanidae; Homo.

1 (bases 1 to 759)

1 (bases 1 to 759)

Rarnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.
Secreted proteins and nucleic acids encoding them
Patent: JP 2002539773-A 54 26-NOV-2002;

MILLENNIUW PHARMACEUTICALS INC

OS Homo sapiens (human)
PN JP 2002539773-A/54

PD 26-NOV-2002
PF 01-MAR-2000 JP 2000602247
PR 01-MAR-1999 US 60/122458
PI THOWAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C PI FRASER
PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68, PC G01N33/15, G01N33/53,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC Secreted proteins and nucleic acids encoding them FH Key
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               AGCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCAGCTGG 941
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 AGCCCCCACCCTACCAGGCCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGG
                                                        ATCCGTACCTGCAGCACGAGATCGACCTGCCRCCCACCATCTCGCTGTCAGACGGGGAGG
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Location/Qualifiers
1..759
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 0;
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, 8	gg Q	Query Ma Best Loc Matches	source	555 TTTD 50		COMMENT	REFERENCE AUTHORS TITLE JOURNAL	ORGANISM	ACCESSION VERSION KEYWORDS SOURCE	RESULT 23 BD272534 LOCUS DEFINITION	Db	g b.	S B	Qy Qy	Qy Qy	Qy Db Qy
582 TGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGGCACA 641	522 CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGG 581	Match 53.1%; Score 701; DB 6; Length 753; Local Similarity 99.9%; Pred. No. 0; Les 751; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68, PC G01N33/15,  PC G01N33/50,G01N33/53,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC Secreted proteins and nucleic acids encoding them FH Key Location/Qualifiers  FT source /organism='Homo sapiens (human)'.	20	MILLENIUM PHARMACEUTICALS INC OS Homo sapiens (human) PN JP 2002539773-A/43 PN 26-NOV-2007	1 (bases 1 to 753) Barnes, T.M., Holtzman, D.A., Secreted proteins and nucle Secreted proteins and nucle Patent: JP 2002539773-A 43	-		BD272534 753 bp DNA linear PAT 17-JUL-2003 N Secreted proteins and nucleic acids encoding them.	725 AAGAGAAGGATAAACAGAAAGGACACCCTCTCTAG 759	665 AGGGGACCCGGCTCCACCACACACACACCCCCCCTAGAGAGCGCAGCCATCTGGAGCA 724 1242 AAGAGAAGGATAAACAGAAAGGACACCCTCTCTAG 1276	605 GCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGGAGCAGTGGGCGCCCCTCCTTGCTGG 664  1182 AGGGGACCCGGCTCCACCACACACACACGCGCCCCTAGAGAGCCGCCCAGCCATCTGGAGCA 1241	545 CGTGCTACGGCAGCGGCGCATGGAGGGCCGCCGCCCACCTACACAGCGAGGTCATCG 604  1122 GCCACTACCGGGGGCTCCTCCTTCCAGCACCAGCAGCAGTGGGCCGCCCTCCTTGCTGG 1181	485 TGGATAGTGCCAGGCTGGGCGCCCCTGCCCCCCAGCAGTAACTCGGGCAACAGCGCCA 544  1062 CGTGCTACGGCAGCGGCGCGCCATGGAGGGGCCCCCCCCC	942 AACTGAACCGGGAGTCGGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 1001
		COMMENT	REFERENCE AUTHORS TITLE	DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 24 BD272495	Qy 12 Db 7	Oy 11 Db 6	Оу 11 рь 6	Qy 106 Db 54	Оу 100 Db 48	Qy s	Qу 8 Дъ з	Qy 8: 3	Qy 7	Qy .7 Db 1	рь Оу 6 рь 1
PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68, PC G01N33/15,	PF 01-MAR-2000 JP 2000602247  PR 01-MAR-1999 US 60/122458  PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C  PI FRASER	MILLENNIUM PHARMACEUTICALS INC OS Homo sapiens (human) PN JP 2002539773-A/4 PD 26-NOV-2002	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 756)  Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C. Secreted proteins and nucleic acids encoding them Patent. JP 2002539773-A 26-NOV-2002;	t o		942 AAGAGAAGGATAAACAGAAAGGACACCCTCTC 1273	B2 AGGGGACCCGGCTCCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCA 1241 	122 GCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGG 1181	)62 CGTGCTACGGCAGCGGCGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCG 1121	002 TGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCGGCA 1061 	942 AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 1001 	B2 AGCCCCACCCTACCAGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCAGCTGG 941	122 ATCCGTACCTGCAGCACGAGATCGACCTGCCACCACCATCTCGCTGTCAGACGGGGAGG 881	762 ACCGCCTGGCCGTGCCGCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCT 821	702 GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG 761	62 42 22

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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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1 (bases 1 to 969)

Barnes, T.M., Holtzman, D.A.,
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BD272515.1 GI:33082283
JP 2002539773-A/24
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                                                                        AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA
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                                         TGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCA 1061
                                                                                                                                                       AGCCCCCACCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGG
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Secreted proteins and nucleic acids encoding them
Patent: JP 2002539773-A 24 26-NOV-2002;

NAL Patent: JP 2002539773-A 24 26-NOV-2002;

COS Homo sapiens (human)
PN JP 2002539773-A/24
PD 26-NOV-2002
PP 01-MAR-2000 JP 2000602247
PP 01-MAR-1999 US 60/122458
PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRIST PI FRASER
PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1, PC G01N33/15,G01N33/50,G01N33/53
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
C G01N33/50,G01N33/53,G01N33/53,G01N33/566,C12N15/00,C12N5/00
Secreted proteins and nucleic acids encoding them FH Key
Location/Qualifiers
                                                                                                                                                                              JP 2002539773-A/24
26-NOV-2002
20-NOV-2000 JP 2000602247
01-MAR-2090 JP 2000602247
01-MAR-1999 US 60/122458
THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER
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REFERENCE
AUTHORS
TITLE
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                                             TGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA
GCCAGGGGGGGAGAGAGAAGATGCCCTGTCCTCAGACGGATGCCTGTGGCCCTCGGAGA
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                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins and nucleic
                                                                                                                                                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                          Location/Qualifiers
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Pred. No. 0;
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DEFINITION
                                                                                                                                                                                                                                                                                    AUTHORS
Hominidae; Homo.

1 (Dases 1 to 1060)

Strausberg RL, Feingold RA, Grouse LH, Derge JG, Klausner RD, Strausberg RL, Feingold RA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Many JJ, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abrameon RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fabey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
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                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 59 Row: m Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 40317614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Alkesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri, Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Sequencing Center (NISC),

Sequencing Center (NISC)
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
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                                                                                            /translation="MAELEFVQIIIIVVVMVVVVITCLLSHYKLSARSFISWHSQG
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49.0%;
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       Score 647; DB 8;
Pred. No. 2.3e-310;
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       REFERENCE
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Homo sapiens (human)
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Sequence 14876 from Patent
CQ728942
                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
Venter, C.J., Adams, M.C.,
                                             Hominidae; Homo.
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                                                                      Craniata; Vertebrata; Euteleostomi; pglires; Primates; Catarrhini;
  Myers, E.W.
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DEFINITION
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Patent: WO 02068579-A 14876 06-SEP-2002;
PE Corporation (NY) (US)
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1 (bases 1 to 61505)
Rae, F.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.
Identification and characterization of a novel gene,
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                    Homo
                                                                                                                                                     AF305426.1 GI:15824468
                                                   Hominidae; Homo.
                                                                                                                    Homo sapiens (human)
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                                                                                                  sapiens
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 1.7e-283;
Matches 593; Conservative 0; Mismatches 0;
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Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A.
Direct Submission
Submitted (13-SEP-2000) Centre for Molecular Biotechnology,
Queensland University of Technology, 2 George St, Brisbane,
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                        TCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAGAGAGAAGGATAAACAGAAAGGACACC
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IIIVVNMVWMVVVITCLLSHYKLSARSFISHISQGRRREDALSSEGCLWPSESTYSGN
IIIVVNMVWDFPACHENLAVPFFAQRERFHRFQPTYPYLOHEIDLPFTISLSOBEEPPF
GIPETQVJAPPRPTDRLAVPFFAQRERFHRFQPTYPYLOHEIDLPFTISLSOBEEPPF
YQGPCTLQLRDDEQQLELNRESYRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATC
YGSGGRNEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWS
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/protein id="AAL09357.1"
/db_xreff"GI:15824469"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="20"
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join(321. .429,50206. .50360,56817. .56870,
gene="STAG1/PMEPA1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone request@sanger.ac.uk
On Dec 5, 2000 this sequence version replaced gi:10198628.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HS718J7

HS718J7

Human DNA sequence from clone RP4-718J7 on chromosome
20q13.31-13.33 Contains the PCKI gene for soluble
phosphoenolpyruvate carboxykinase 1, the ZBP1 gene for Z-DNA
binding protein 1, the 3' end of the TMEPAI gene for transmembrane
prostate androgen induced mRNA, two putative novel genes, the 5'
end of the CTCFL gene for CCCTC-binding factor (zinc finger)-like
                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL035541.15 GI:11546043
HTG; C20orf183; CpG island; CTCFL;
phosphoenolpyruvate carboxykinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Wellcome Trust Sanger Institute Center code: SC Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20 RP4-718J7 is from the library RPCI-4 constructed by the group of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sehra,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; ZBP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VECTOR: PCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                         _type="genomic
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PMEPA1; TMEPAI; transmembrane
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                                                                polyA_site
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39408. 39570,40012. .40236,40325. .40456,40883. .40978,
41193. .41647)
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complement (AL160176.3:45247...41443),
complement (AL160176.3:36091...36256),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (AL160176.3:55723.55933),
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complement (AL160176.3:29827.
                                                     TAHLPDRREIISFGSGYGGNSLLGKKCFALRMASRLAKEEGWLAEHMLILGITNPEGE
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Best Local Similarity
Matches 593; Conserv
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                       789
AGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCCTGCAGCACGAGATCGACC
                                                                                   AGCCGCAGGTCTACGCCCCGCCTCGGCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCC
                                                                                                                                      Conservative
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complement (join(<75750. .76071,76755. .77015))

/locus_tag="RP4-718J7.4-001"

complement (join(<75750. .76071,76755. .77015))

/locus_tag="RP4-718J7.4-001"
                                                                                                                                                                                                                                                                                                                                            /translation="maqapadpgreghleqrilqvlteagspyklaqlvkecqapkrelnqvltrakspareqchaptipetpg loqvlyrmkkelkvsitspatmyclggtdpeggreaelalsspareqchaptipetpg pgpsgpalialsspareqchaptipetpg pgpsgpalviaqalgmriakdvurdlyrmksrhlldndegsk awtiyrpebgsraksasiiychmylimicqnsqpnshisianseaiqichgniitrqt vsredgsgrraksasiiychgrupimigcoldimeqsilrrvqlghsnemrlhg vsredgsagprhipsgmapgdsstwgtlvdpwgpqdihmeqsilrrvqlghsnemrlhg vpsegpahippgspysataagpeaspearipspgthpegaaaripagpaagrihkscfhedati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus tag="RP4-718J7.1-001"
complement(join(80416. .80612,85992. .86210,87570. .8777
89006. .89173,90730. .90903,91355. .91423,92087. .92311,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   match: cDNAs: AJ300575.1" complement (79689)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /\textrm{Tocus_tag="RP4-718J7.1-001"}.complement(join(79689. .80612,85992.complement(join(79689. .80612,85992.89066. .89173,90730. .90903,91355. .96105. .96316))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=\text{match: ESTs: BE408987 BE890965 BE893630"}

complement(join(79689. .80612,85992. .86210,87570. .8777

89006. .89173,90730. .90903,91355. .91423,92087. .92311,
                                                                                                                                                                                                                                                                                       GNSNKMSISPGVAGPGGVAGSGEGEPGEDAGRRPADTQSRSHFPRDIGQPITPSHSKLTPKLETMTLGNRSHKAAEGSHYVDEASHEGSWWGGGI"
complement(join(88734. .89173,90730. .90903,91355. .92311,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus_tag="RP4-718J7.1-001"
complement(79706. .79711)
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/locus_tag="RP4-718J7.5-001"
/locus_tag="RP4-718J7.5-001"
/locus_tag="RP4-718J7.5-001"
                                                                                                                                                                                                             complement (join (88734. .89173, 90730. .90903, 91355.
                                                                                                                                                                                                                                                                                   complement (join (88734.
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/locus_tag="RP4-718J7.1-002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: proteins: Q8VDA5 Q8VE02 Q9H171 Q9QY24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein_id="CAI23107.1"
/db_xref="GI:56203061"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard_name="OTTHUMP00000031373"
                                                                                                                                                    44.9%;
100.0%;
                                                                                                                                                Score 593; DB 8; Le
Pred. No. 1.7e-283;
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560; Conserv
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Sequence 32 from Patent W00242776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sun,Y., Recipon,H., Chen,S.Y. and Liu,C. Compositions and methods relating to prostate specific genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCCACCCACCATCTCGCTGTCAGACGGGGAGCGCCCCCACCCTACCAGGGCCCCTGCA
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GCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCAC 909
                                                                    GCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCT 849
                                                                                                                                   GCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCA
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                                            GCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCT
                                                                                                                                                                                                                          42.4%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="unassigned DN
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SD)
                                                                                                                                                                                                                            0;
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Pred. No. 4.6e-267;
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                                                                                                                                                                                      Direct Submission

AL Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

On Mar 6, 2000 this sequence version replaced gi:7007305.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20

REPS-1059L7 is from the library RPCI-5 constructed by the group of Private To Town Sanger.ac.uk/HGP/Chr20
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AL121913.4 GI:7161781
AL121913.4 GI:7161781; TMEPAI; transmembrane protein.
HTG; CpG ' - 'hwman'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DNA sequence from clone RP5-1059L7 on chromosome 20q13.2-13.33 Contains the 5' end of the TMEPAI gene for transmembrane prostate androgen induced mRNA, ESTs, STSs, two CDG islands, complete sequence.
                                               Web site:
                                                                 Center code: SC
                                                                                     Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skuce, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                VECTOR: PCYPAC2
                                                                                                                                                                         Pieter de Jong. For further details see
                        Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCA 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACC 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTCTAGGGTCCCCAGGGGG 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAGAAGGATAAACAGAAAGGACACCC 1269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGGGGCGCATGGA 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTG 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGGAGTCGGTGCGCGCACC 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 150224)
                                                                                                                                                       //www.chori.org/bacpac/home.htm
                                             http://www.sanger.ac.uk
                                                                                                              Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150224 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSSs and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
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                                                                                                              SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="q13.2-13.33"
/clone="RP5-1059L7"
/clone_lib="RPCI-5"
                                                                                                                                       AF305616"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="TMEPAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="TMEPAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="TMEPAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="TMEPAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="TMEPAI"
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
join(complement(52376. .52484),complement(2445.
complement(AL035541.15:128876. .128929),
complement(AL035541.15:127896. .128441))
                                                                                                                                                                                                   AA126999 AA128075 AA144094 AA200476 AA204175 AA208809
AA229168 AA249792 AA260038 AA310984 AAA22316 AA432556
AA435292 AA482527 AA485591 AA487031 AA512956 AA523925
AA535281 AA535262 AA535819 AA536113 AA541675 AA570597
AA595115 AA606959 AA611168 AA616366 AA632457 AA652239
AA658276 AA689679 AA815501 AA917446 A1142707 A1150565
A1152331 A1154451 A1154781 A1159482 A1181338 A1250993
A1152331 A1154451 A1154781 A1159482 A1181338 A1250993
A1272934 A1336269 A1369306 A1374498 A1381990 A1381391
A1466182 A1467828 A1493698 A1594390.1 A1640802 A1673419
A1677810 A1742327 A1761441 D57097 N64192 N71820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(complement(52376. .52804),complement(2445.complement(AL035541.15:128876. .128929),complement(AL035541.15:124241. .128441))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(complement(52376. .52804),complement(2445.
complement(AL035541.15:128876. .128929),
complement(AL035541.15:124241. .128441))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(complement(53362. .53365), complement(2445. .2599),
complement(AL035541.15:128876. .128929),
complement(AL035541.15:127896. .128441))
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join (complement (53362. ..53425), complement (2445.

complement (AL035541.15:128876. .128929),

complement (AL035541.15:127622. .128441))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="maelefvQIIIIVVVmmvmvvVVITCLLSHYKLSARSFISRHSQG
RRREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHRFQPTV
PYLQHEIDLPPTISLSDGEEPPPYQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSD
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match: cDNAs: AF224278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMDSARLGGPCPPSSNSGISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus_tag="RP4-718J7.3-001"
/note="match: ESTs: AA027926 AA088701 AA104273 AA122026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard_name="OTTHUMP00000031380"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                locus_tag="RP4-718J7.3-001"
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                                                                                                                                                                             AF009425
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RESULT 33
AX071267
LOCUS
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                                                                                      DEFINITION
ACCESSION
                                            SOURCE
                                                           KEYWORDS
                                                                         VERSION
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                              ORGANISM
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                                                                         Sequence 17:
AX071267
AX071267.1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                              Homo
                                            Homo
                                                                                                                      AX071267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGACCGCGGTCTCGGAGCGAAACCCGATCTCCTTGGACTTGAATGAGGAGGAGGAGGAGGCGG
                                                                                                                                                                                                                GTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCGCACCCCCCCCCCCCCCACCCCATTTTCCCGGACCCCACCCCGGGCACTGCCG
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                                                                                                                                                                                                                                                                               CTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGCCGGCAGCCCAATGTCTCCTGCAC 480
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                                                                                                                                                                                                  GTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCA 52376
                                                                                                                                                                                                                                                             CTCCCCGCCGCGCGCCTCCTGCATGCGGGGCCCCCAGCTCCGGGCGCCGGAGCCCC
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ilarity 100.0%;
Conservative (
                            sapiens
                                            sapiens (human)
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/broteIn_id="CAI19031.1"
/db_xref="G1:56203336"
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/translation="MHRLMGUNSTAAAAAGDENVSCTCNCKRSLFQSMEITELEFVQI
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YQGPCTLQLRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATC
                                                                                                         1739 from Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(2452. .2599,54226. .54438))
/gene="TMBPAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /locus_tag="RP4-718J7.3-003"
complement(join(2452. .2599,54226. .54438))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWS
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                                                                           GI:12581618
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                                                                                                                        DNA
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SOURCE
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AX392430/c
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ORIGIN
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Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
Labat,I., Leshkowitiz,D., Kita,D., Garcia,V. and Strache-Crain,B.
Human genes and gene expression products
Patent: WO 0102568-A 1739 11-JAN-2001;
CHIRON CORORATION (US); HYSEQ, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams, L.T.,
                                                                                   Diagnosis and treatment of cardiovascular conditions Patent: WO 0216416-A 14 28-FEB-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER Location/Qualifiers
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                     Sequence 14 from Patent WO0216416.
                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                     AX392430.1
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                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                             Turi,T.G.
                                                                                                                                                                          Lee,R.T., Landschulz,K.T.,
                                                                                                                                                                                                               iominidae;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
              /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                        GI:19700746
                                                                      . 693
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Pred. No. 6.5e-188;
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                                                                                                                                                                            Kennedy, S.P.,
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ACCESSION
VERSION
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BD226320
LOCUS
                                                                                              ORIGIN
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Query Match
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Matches 321; Conserva
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Best Local Similarity
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                                                                                                                                                                                                                              PARCTECIC, CANCER LISSUE-ORIGIN human nucleic aci Patent: JP 2002512795-A 105 08-WAY-2002;
PATENTE GESELLSCHAFT FUER GENOM FORSCHUNG MBH OS Homo sapiens (human)
PN JP 2002512795-A/105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1125
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pancreatic cancer tissue-origin human BD226320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Specht, T., Hinzmann, B., Schmitt, A., Pilarsky, C., Dahl, E. and Rosenthal, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP 2002512795-A/105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGG 1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286
  Conservative,
                                                                                                                                                                                                                                                                                 C12N5/10,C12P21/02,C12P21/08,C12N15/00,A61K37/02,C12N5/00 reatic cancer tissue-origin human nucleic acid sequence FH Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 EDGAR DAHL,
ANDRE ROSENTHAL
C12N15/09,A61K38/00,A61K48/00,A61P1/18,A61P35/00,C07K14/435,
                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-1999 JP 2000546002
28-APR-1998 DE 198 20 190.7
THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY
                                                                                                                                                                                                        /organism='Homo
Location/Qualifiers
                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                   20.5%;
  0,
  Score 271; DB 6; Pred. No. 3.4e-123; 0; Mismatches 1;
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                                             Length 812;
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AX011709
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Human nucleic acid sequences obtained from pancreas tumor tissue Patent: WO 9955858-A 107 04-NOV-1999;
SCHMITT ARVIN (DE); SPECHT THOWAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)
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                                                  GCCTGGCCGTGCCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCTATC
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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Pred. No. 3.4e-123;
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Rosenthal, A.

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Sequence 172
CQ976481
CQ976481.1
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Einstein,R., McGowan,K.M. and Pando,M.P. Prostate specific genes and the use thereof cancer therapy and diagnosis Patent: WO 2004113571-A 172 29-DEC-2004; Exonhit Therapeutics S.A. (FR)
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Prostate specific genes and the use thereof
cancer therapy and diagnosis
Patent: WO 2004113571-A 170 29-DEC-2004;
Exonhit Therapeutics S.A. (FR)
Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                           Hominidae; Homo.
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ilarity 100.0%;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                        GCACAGTGTCAGGCAACGGAATCCCAGAG
                                                                                                                                                                                                                       CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGG
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                       GCACAGTGTCAGGCAACGGAATCCCAGAG
                                                                                GCCAGGGGGGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA
                                                                                               GCCAGGGGGGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA
                                                                                                                                         TGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA
                                                                                                                                                          TGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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100.0%; Pr
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Pred. No. 2.5e-92;
0; Mismatches 0;
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Pred. No. 2.5e-92;
0; Mismatches 0;
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WO2004113571.
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Gaps

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CQ735730
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AUTHORS
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ORGANISM
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CQ976480/c
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Best Local Similarity
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                Query Match
Best Local :
                                                                                                                                                       JOURNAL
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 Matches 110;
             Local Similarity
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Prostate specific genes and the use thereof
cancer therapy and diagnosis
Patent: WO 2004113571-A 171 29-DEC-2004;
Exonhit Therapeutics S.A. (FR)
                                                                                                                                                                                                                                                                                                                            CQ735730
Sequence 21664 from Pat
CQ735730
CQ735730.1 GI:42328620
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                                                                                                                                                                    Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and oth thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                          Patent: WO 02068579-A 21664 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                    Homo sapiens
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Mammalia; Eutheria;
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Conservative
                                                                   /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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             8.3%;
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Score 110; DB 6;
Pred. No. 4.7e-43;
0; Mismatches 0;
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WO2004113571.
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WO02068579.
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REFERENCE
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CQ543985
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VERSION
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CR956367/c
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KEYWORDS
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Sequence
CQ543985
                                                                                                                                             Harley, J.

Direct Submission

Direct Submission

Submitted (05-AUG-2005) Wellcome Trust Sanger Institute, F

Submitted (05-AUG-2005) Wellcome Trust Sanger Institute, F

Cambridgeshire, CB10 ISA, UK. E-mail enquiries: vega@sanger

Clone requests: clonerequest@sanger.ac.uk

On Jul 9, 2005 this sequence version replaced gi:68659251

On Jul 9, 2005 this sequence replaced gi:68659251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shoshan,A., Wasserman,A., Mintz,E., Mintz, Oligonuclectide library for detecting rna variants that populate a transcriptome Patent: WO 0210449-A 13620 07-FEB-2002; Compugen Inc. (US)
Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa chromosome 2 unordered pieces.
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60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                    Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
----- Project Information
                                                                                                                      Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                                          SuB.
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                           Sus scrofa
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                    Center project name: bT122C21
                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (pig)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.5%;
Conservative
'AGCCA'''
                                                                                                                                                                                                                                                                       (bases 1 to 158243)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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17 clone
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ne PigE-122C21,
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.o. 3.7e-18;
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                                                                                                                                                                                                        vega@sanger.ac.
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DRAFT SEQUENCE,
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                                                                                                                                                                                                                                                                                                             Suidae;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 158143; sum-of-contigs
Insert size: 16271; 5.4% error; agarose-fp
Quality coverage: 7.74x in Q20 bases; sum-of-contigs Quality
coverage: 7.54x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                 Submitted (09-AUG-2005) Wellcome Trust Sanger Institute, H. Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sange: Clone requests: clonerequest@sanger.ac.uk
On Jul 15, 2005 this sequence version replaced gi:68677383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa chromosome SEQUENCE, 2 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 158077 bases at least Consensus quality: 158115 bases at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 157977 bases at least
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 183108 bases at least Q40
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR956387.4 GI:70908009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CR956387
                                                                                 Center project name: bE148I13
                                                                                                                                                                       Center code: SC
                                                                                                                                                                                           Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                       Sus
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CR956387
                                                                                                                         Contact: vega@sanger.ac.uk
                                                                                                                                                 Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                             Almeida, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGACCGCGTCTCGGAGCGAAACCCCGATCTCCTTGGACTTGAATGAGGAGGAGGAGG 105159
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                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 183457)
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104859. .158243
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9 104858: gap of 100 bp
9 158243: contig of 53385 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment:01841"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="PigE-122C21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:9823"
chromosome="17"
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                                                                                                                                                                                                             ---- Genome Center
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                                                             --- Summary Statistics
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                                                                                                            Project Information
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17 clone C
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CH242-148I13, WORKING DRAFT
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                                                                                                                                                                                                                                                                               nstitute, Hinxton,
vega@sanger.ac.uk
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 TGATGGTGATGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTC 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 495 from Patent WO0151670.
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Consensus quality: 183228 bases at least Q20
Insert size: 183357; sum-of-contigs
Insert size: 194085; agarose-fp
Quality coverage: 6.06x in Q20 bases; sum-of-contigs Quality
coverage: 5.80x in Q20 bases; agarose-fp
                                                                                                                                                                           methods of use thereof
Patent: WO 0151670-A 495 19-JUL-2001;
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                               Nucleic acids containing single nucleotide polymorphisms and
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                 AX199565.1 GI:15389996
                                                                                                                                                                                                                                                     Shimkets, R.A. and Leach, M.D.
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                         Curagen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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/mol_type="genomic DNA"
/db_xref="taxon:9823"
/chromosome="17"
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clone_end:SP6
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/note="assembly_fragment:00014
fragment_chain:1"
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                  /note="1 of 2 allelic variants (496 is other entry)
accession number cg42747251"
                                                                                              /organism="Homo sapiens"
/mol_type="unassioned DN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                       /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="assembly_fragment:00884
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clone_lib="CHORI-242"
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90451: gap of 100 bp
183457: contig of 93006 bp in length
                                                                                                                                                       tion/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52; DB 14; 1; Pred. No. 3.5e-14;
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REFERENCE
AUTHORS
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TITLE
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BD272546
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Matches 51
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.
Secreted proteins and nucleic acids encoding them
Patent: JP 2002539773-A 56 26-NOV-2002;
MILLENNIUM PHARMACEUTICALS INC
OS Mus sp. (mouse)
PN JP 2002539773-A/56
PD 26-NOV-2002
PF 01-MAR-2000 JP 2000602247
PF 01-MAR-1999 US 60/122458
PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRI.
PI FRASER
PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12PC C13N33/15, C01N33/15 C01N33/15
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BD272546
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                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 484)

Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C. Secreted proteins and nucleic acids encoding them Patent; JP 2002539773-A, 55 26 NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                      BD272546.1 GI:33082314 JP 2002539773-A/55.
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MILLENNIUM PHARMACEUTICALS
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llarity 100.0%; P
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/mol_type="genomic DNA"
/db_xref="taxon:10095"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44;
Pred. No.
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3.4e-10;
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hes 0;
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PD 26-NN
PF 01-NJ
PF 01-NJ
PF 11-NJ
PF 71-NJ
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PN JP 201
PD 26-NOV
PF 01-MAR
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PI THOWAS
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G01N33/15,
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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JP 2002539773-A/44.
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Secreted proteins and nucleic acids encoding them FH Key
Location/Qualifiers
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JP 2002539773-A/55
3.3%; Score 44; DB 6; Local Larity 100.0%; Pred. No. 3.4e-10; Conservative 0; Mismatches 0;
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01-MAR-2000 JP 2000602247
01-MAR-1999 US 60/122458
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01-MAR-1999 US 60/122458
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JP 2002539773-A/44
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feature (1)..(484).
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10095"
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/db_xref="taxon:10095"
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3.4e-10;
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PN JP 2002539773-A/14

PD 1-MAR-2000

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Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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2 (bases 1 to 651)
Jolliffe, C.N. and Kumar, S
Direct Submission
                                                                                                               1 (bases 1 to 651)
Jolliffe, C.N., Harvey, K.F., Haines, B.P., Parasivam, G. and Kumar, S. Identification of multiple proteins expressed in murine embryos as
                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                               Identification of multiple proteins expressed in murine embryos as binding partners for the WW domains of the ubiquitin-protein ligase
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THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C
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AAH17635
ABZ11378
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ADU02022
ADA69463
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ACH91938
ABQ22357
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ABQ39948
ABQ39949
ABA09728
        ADM43896
ADQ20652
ABZ58671
ADB62863
ADQ87086
ADX05558
AAS76375
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ADA24495
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ADP79328
ADP79326
ADX07095
AEB94287
  ABL63316
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Ada69463 Rice gene
Ada71296 Rice gene
Ada71296 Rice gene
Ada71296 Rice gene
Ach91938 Human gen
Abg22257 Oligonucl
Abg22356 Oligonucl
Adg23256 Oligonucl
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Adg79328 Human cas
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Adg7939 Cyclin-de
Adw60939 Eucalyptu
Adm1993 Novel hum
Add19337 Rice stre
Acl36936 Rice stre
Acl36938 Rice stre
Acl36937 Rice stre
Add41376 Plant cDN
Add51086 Plant cDN
Add51086 Plant ful
Aaf44644 Novel human sof
Acc49023 Human mol
Add62397 Human mol
Add62397 Human fon
Add64014 Human con
Add64014 Human con
Add64014 Human con
Add64015 Renal can
Abn59814 Novel hum
Aca4977 Human CDN
Add96445 T cell ac
Add96443 T cell ac
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Add96443 T cell ac
Add96443 T rell ac
Add9644977 Insulin sv
Aac89368 Human org
Adz49774 Insulin s
Aah17635 Human cDN
Abz11378 Human pol
Adm20652 Human sof
Abz58671 Human KNN
Add62863 Human cDN
Add62863 Human tum
Add987086 Human tum
Adx05558 Cyclin de
Aas76375 DNA encod
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                                                                                                                                                          ABK12137;
                                                                                                                          Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1
                                                                                                                                           05-JUN-2002
                                                                                                                                                                         ABK12137
   WO200216416-A2
                                                               Homo
                                                               sapiens.
                                                                                                                                                                                                                                      standard;
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               /*tag= a
/product= "MTVR-1"
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AAS76377
ABD32919
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AAS85031
ACN37313
AAS42183
AAA162831
ABS52757
ADW02014
AEB94294
ABK31220
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AAS61132
AAD31202
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ADQ597960 0
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ABD313754 0
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Best Local Simi
Matches 1321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid molecule encoding Mechanically Induced Vascular Receptor-1 polypeptide, useful for treating cardiovascular diseases.
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CTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGCCGGCAAGTCTCTCCTGCAC
                                                          ACGCCCCGGGGCTGCCGAGGGGAGGCCGGGGGGGGCGCAGCGGAGCGCGGTCCCGCGCAC
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                                                                                      Query Match
Best Local
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immune disorder; neoplasm; colon tumor; gastrointestinal disease;
adenocarcinoma; carcinoma; screening; diagnostic; prognostic;
pharmaceutical; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of classifying the cancer in an individual having contracted cancer, which comprises determining the microsatellite status of the tumor. The microsatellite status or the
                                                                                                                                                               useful for classifying the cancer in an individual having contracted cancer, i.e. colon cancer, e.g. an adenocarcinoma, a carcinoma, a teratoma, a sarcoma, and/or a lymphoma. The present sequence represents colon cancer-associated gene used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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26-NOV-2004;
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                                                           The invention relates to human tumour-associated antigenic target (TAT) copypeptides, and their related nucleic acids. The TAT polypeptides are coverexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptide polypeptides; expression vectors and host cells comprising a TAT nucleic acid, an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT nucleic acid, an antibody specific for a TAT polypeptide; are set acids, and the set and methods and compositions for the treatment or antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder across system, melanoma and leukaemia. TAT nucleic acids may further be used as bystem, melanoma and leukaemia. TAT nucleic acids may further be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
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    used as hybridisation probes, in chromosome and gene mapping, chromosome identification and in gene therapy. The present se represents a TAT nucleic acid of the invention
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20-NOV-2001;
02-JAN-2002;
03-APR-2002;
19-AUG-2002;
ACC49493 to ACC49552 encode the human tumour-associated antigenic target (TAT) proteins given in ABP97175 to ABP97234. The present invention describes an isolated antibody that binds to a polypeptide having at least 80 % sequence identity to any of the 60 150-800 residue amino acid sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking its associated signal peptide, encoded by any of the 60 2000-3000 base
                                                                                                                                                                       New antibodies against tumor-associated antigenic target polypeptide, useful for treating or diagnosing tumors or cancers in mammals, e.g. prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
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gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of the comprises of the comprise of
                                                                                                                                                                                                                                    The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and the state of th
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CC genes for targeting in the treatment of rheumatoid arthritis in a mammal CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an CC array or gene chip, specific for rheumatoid arthritis; diagnosis or CC analyses of autoimmune disease or rheumatoid arthritis; screening the CC efficacy of a candidate drug in vitro for the treatment of collagen-CC induced arthritis; and reducing the symptoms associated with collagen-CC induced arthritis; and reducing the symptoms associated with collagen-CC antigout, antiinflammatory, dermatological, antiarthritic, osteopathic, CC antigout, antiinflammatory, dermatological, and immunomodulatory. The CC methods and compositions of the present invention are useful for CC diagnosing and treating autoimmune disease or arthritides, such as CC represents a DNA sequence gout, juvenile rheumatoid arthritis, and an CC immune disease caused by an infectious agent. This polynucleotide contents a DNA sequence relating to the genes used in the analysis and CC treatment of autoimmune diseases or arthritides. Note: This sequence is CC treatment of sequence relating to the genes used in the analysis and contents from in the specification. It has been supplied in an electronic
                                                        from WIPO.
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4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other,

Query Match Loca1

Similarity

93.0%;

Score 1229; Pred. No. 0;

DB 11;

Length

4839;

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Matches 1229; 121 213 453 301 393 241 333 181 273 153 61 93 44 TTCCGGACGCCACCCGCGGCACTGCCGACGCCCCCGGGGCTGCCGAGGGGAGGCCGGGG TTCCGGACGCCACCCGCGGGCACTGCCGACGCCCCCGGGGGCTGCCGAGGGGAGGCCGGGG CCCAGCTCCGGGCGGCCGGAGCCCCCCCGGGCCCCCGAGCCCCCCGCGCCCCCGC GACCCGAGCCGGCGAGCCGGGGGGGGGCCTCCTGCATGCGGGGC GGGCGCAGCGGAGCGCGCTCCCCGCGCACTGAGCCCCCGGGCGCCCCCGGGAACTTGGCGGC CCGCCGGGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCA GCCGCGCCGCCGCCCTCCATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCG GCCGCGCCGCCGCCGTCCATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCG Conservative <u>.</u> Mismatches 0; Indels 0, Gaps 272 512 180 120 332 212 60 360 452 300 392 240

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TGGAGATCACGGAGCTGGAGTTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGA

CCGCCGGGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCA

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CCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTC

GCCGGCACAGCCAGGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGC

692 540 632 480 572 420

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TGGTGGTGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCA TGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCA TGCAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGA

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Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and tre-
                                                                                                                                                                    Hirsch R,
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rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and

English

CC patient sample containing mRNA, analysing gene expression using the mRNA CC that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease CC or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention CC further comprises: a treatment of rheumatoid arthritis; identification of Genes for targeting in the treatment of rheumatoid arthritis; in a mammal containing the containing the containing the efficacy of a candidate drug in vitro for the treatment of collagency induced arthritis; and reducing the symptoms associated with collagency induced arthritis; and reducing the symptoms associated with collagency induced arthritis; and reducing the symptoms associated with collagency induced arthritis; and reducing the symptoms associated with collagency antigout, antinfilammatory, dermatological, and immunomodulatory. The compositions of the invention have the following activities and treating autoimmune disease or arthritides, such as rheumatoid arthritis, lupus, antylosing spondylitis, fibrositis, contemparation and infectious agent. This polynucleotide in the analysis and creatment of autoimmune diseases or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic content format from WIPO. disease or relates to a novel method for diagnosing and analysing sease or arthritides. The method comprises obtaining a containing mRNA, analysing gene expression using the mRNA

Sequence 4839 BP; 1103 A; 1313 ç; 1290 G; 1133 T; 0 U; 0 Other;

93.0%;

BB 11;

Length

4839;

Ś 밁 8 밁 δ 밁 S 뭐 S 밁 Ś 밁 5 밁 5 맑 Ś Query Match Best Local S Matches 1229 cal Similarity 1229; Conserv 301 333 181 121 481 573 421 361 453 393 241 273 213 153 61 93 GCCGCGCCGCCGCCGCCATCCATGCACCGCTTGATGGGGGGTCAACAGCACCGCCGCCGCCG GACCCGAGCCCGGCGAGCCGGGGGGGCGCCTCCCCCGCCGCGCGCCCTCCTGCATGCGGGGC GGGCGCAGCGGAGCGCGCTCCCGCGCACTGAGCCCCCGGGGCGCCCCGGGAACTTGGCGGC GGGCGCAGCGGAGCGCGGTCCCGCGCACTGAGCCCCGCGGCGCCCCCGGGAACTTGGCGGC TTCCGGACGCCACCCGCGGGCACTGCCGACGCCCCCGGGGCTGCCGAGGGGAGGCCGGGG TTCCGGACGCCACCCGCGGGACTGCCGACGCCCCCGGGGCTGCCGAGGGGAGGCCGGGG GGAAAGCTAGCGGCAGAGGCTCAGCCCCGGCGGCAGCGCGCCCCGCTGCCAGCCCATT TGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCA TGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCCTGGTGGTGATGATGATGATG CCGCCGGGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCA TGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCA TGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGA GCCGCGCCGCCGCCGTCCATGCACCGCTTGATGGGGGT Conservative 100.0%; 0 Score 1229; Pred. No. 0; Mismatches 0 Indels 0 Gaps 632 512 452 392 240 332 180 272 120 212 60 540 480 572 420 360 0

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                                                                                                                                                                                                                                        ADM67045 standard;
                                                                                                        antidiabetic;
                                                                                                                             human, adipocyte specific; ds, adipose tissue, anti-obesity; high mobility group I-C protein; HMGI-C; obesity; leptin: ob
                                                                                                                   adipogenesis;
             29-JUL-2003; 2003WO-US023684
                                                           WO2004011618-A2
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                                                                                                                   group I-C protein; HMGI-C; obesity; leptin; ob; diabetes; hypertension; cardiovascular disease; anorectic;
                                                                                                         hypotensive.
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212 60

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Best Local Similarity Matches 1229; Conserv

Conservative

93.0%; Score 1229; 1 100.0%; Pred. No. 0; tive 0; Mismatches

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Sequence 4839 BP; 1103 A; 1313 C; 1290 G;

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421

453 301 393 241 333 181 273 121 213

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This invention relates to a novel method for identifying genes that are cover-expressed in adipose tissue and as such it provides targets for anti cobesity pharmaceutical compositions. Specifically, it refers to a high combility group I-C protein (HMGI-C) that is associated with obesity and cis epistatic to leptin, furthermore, it refers to the ob gene where an composition of the performing differential gene expression analysis cinvention describes performing differential gene expression analysis cof any two different mice selected from a group consisting of wild-type, compounds that are adipocyte specific, and as such can be used for the differential gene expression analysis contentified that are adipocyte specific, and as such can be used for the differential gadipogenesis, diagnosing and treating diabetes, obesity, compounds that can modulate or prevent adipogenesis and treat diabetes or compounds that can modulate or prevent adipogenesis and treat diabetes or obesity. These compositions exhibit anorectic, antidiabetic and compounds adipocyte specific DNA sequence is a human homologue of a murine adipocyte specific DNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying adipocyte specific genes, useful for treating obesity or diabetes, and for identifying drug targets, by differential gene expression analysis between adipose tissue or stromal vascular tissumice of different genotypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-2002; 2002US-0398785P.
12-JUN-2003; 2003US-0478206P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; SEQ ID NO 180; 91pp; English.
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22-FEB-2004; 2004WO-DE000433.
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                                                                                                                                                                                                                                                             human; cytostatic; diagnosis; prostatic
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GGGCGCAGCGGAGCGCGCTCCCGCGCACTGAGCCCCGCGGCGCCCCGGGAACTTGGCGGC

180 272 120 Matches Query Match

93

153 61

> TTCCGGACGCCACCCGCGGCACTGCCGACGCCCCCGGGGCTGCCGAGGGGAAGGCCGGGG

TTCCGGACGCCACCCGCGGGCACTGCCGACGCCCCGGGGGCTGCCGAGGGGGAGGCCGGGG

Local 1229;

Similarity

93.0%;

Score 1229; Pred. No. 0; Mismatches

DB 13; 0,

Length 4839; Indels

0

Gaps

0

60 212

Conservative

0;

Sequence

4839

BP; 1103 A;

1313 C; 1290 G; 1133 T; 0 U; 0 Other;

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This invention describes novel cytostatic polynucleotide and polypeptide cor the risk of developing prostatic cancer. Diagnosing prostatic cancer determining over transcription or over expression of the sequences in compositatic tissue. Screening for inhibitors of the sequences in compositatic tissue. Screening for inhibitors of the sequences or detection compositatic tissue. Screening for inhibitors of the sequences or detection compositatic tissue. Screening for inhibitors of the sequences or detection composited that bind are composited that bind are composited to the presence of the sequences in composite that bind are composited that bind are composited to the presence of the sequences in composite that bind are composited to the presence of the presence of the composite that binds that binds that binds to the presence of composite the presence of the sequences of the sequences of the sequences of the sequences of the polypeptide, preferably 300, that binds to the polypeptide; an composite the polypeptide; an antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotype, non-human composited that reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polymucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that composite the sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained semples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and colour invention.
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Schmitt A, s
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14-MAY-2003;
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PILARSKY C.
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3, Bruemmendorf T, Kinnemann
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Sequence 4839

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Schmitt A,
Xinzhong L,
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PILARSKY C.
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                                            pronchial cancer comprising 489 defined sequences given in the great production. The invention may be useful for the production of compounds with a cytostatic activity through the inhibition of expression or activity of tumour-associated proteins. The novel DNA sequences and the proteins/peptides encoded by them are used for detecting bronchial cancer or determining the risk of developing it and to screen for specific binding partners of the DNA or protein sequences, where the binding partners are potentially useful as agents for treating or diagnosing bronchial cancer. The DNA or protein sequences can also be used for prognosis, detection of metastases and for secondary treatment (of tumours that have been stabilised or are no longer detectable). Ce teacting abnormal expression of the DNA sequences provides early diagnosis of bronchial cancers. The present sequence is that of a novel bronchial cancer-associated human gene sequence of the invention.
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Sequence 4839 BP; 1103 A; 1313 C; 1290 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a novel isolated nucleic acid associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 285; 1381pp; German.
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Li X, Roepcke
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DB; ADU06550.
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e S, Staub E, Hinzmann
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Query Match

93.0%;

Score 1229;

DB

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Length 4839;

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1113 AGGTCATCGGCCACTACCCGGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCT 1172	CAGCGCCACGTGCTACGGCAGCGGCGGG	1053 TCAGCGCCACGTGCTACGGCAGCGGCGGGGGGCGCATGGAGGGGCCGCCGCCGCCCTACCTA	993 GTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCA 1052	933 AGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACA 992 	CGAGC 9	STCAG 78	53 GGCCACCGACCGCCTGGCCGGCCCTTCC 81 [	GCCCCGCCTC 75	GCCCTGTCCTCAGAAGGATGCCT( 	TTCATCA 63	513 TGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGGTGATGATGGTGA 572	r) 4.	393 GCCGCGCCGCCGCCGTCCATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCG 452	333 CCCAGCTCCGGGCCGGCCGGAGCCCCCCCGGCCGCCCCGAGCCCCCGCGCCCCGC 392	273 GACCCGAGCCCGGCGAGCCCGGGGCGCGCCCCCCGCGCGCGCCTCCTGCATGCGGGGC 332	213 GGGCGCAGCGGAGCGCGGTCCCGCGCACTGAGCCCCGGGGGCGCCCCGGGAACTTGGCGGC 272	153 TTCCGGACGCCACCCGCGGGACTGCCGACGCCCCCGGGGCTGCCGAGGGGAGGCCGGGG 212	93 GGAAAGCTAGCGGCAGAGGCTCAGCCCCGGCGGCGGCGGCGCCCGCTGCCAGCCCATT 152	Best Local Similarity 100.0%; Pred. No. 0; Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ДЬ	021
당 :	1081 CCTTGCTGGAGGGGACCCGGCTCCACCACACACACACCCCCTAGAGAGCGCAGCCA 1140
Ş	1233 TCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGGCC 1292
망	1141 TCTGGAGCAAAGAAAGGATAAACAGAAAAGGACACCCTCTCTAGGGTCCCCAGGGGGCC 1200
5	93 GGGCTGGGGCTGCGTAGGTGAAAAGGCAG 132
DЬ	1201 GGGCTGGGGCTGCGTAGGTGAAAAGGCAG 1229
RESULT ADW433	JLT 11 43368 ADW43368 standard; DNA; 4839 BP.
\$ 5 B	ADW43368;
I I X	24-MAR-2005 (first entry)
₽×	Prostate cancer related gene, SEQ ID 166.
<b>XXX</b>	Cytostatic; Gene Therapy; Prostate tumor; prostatic cancer; diagnosis; ds; gene.
88	Homo sapiens.
2 X	WO2004113571-A2.
# # X	29-DEC-2004.
P X	25-JUN-2004; 2004WO-IB002394.
P X	26-JUN-2003; 2003US-0482595P.
PX	(EXON-) EXONHIT THERAPEUTICS SA.
2 2	Binstein R, Mcgowan KM, Pando MP;
\$ <del>2</del>	WPI; 2005-057996/06.
. F. B.	New isolated nucleic acid sequence that is expressed by human prostate cancer cells, useful as target for treating, preventing and/or diagnosing cancers, particularly prostate cancer.
S S	im 1; SEQ ID NO 166; 198pp; English.
CC The CC expl	The present invention relates to novel nucleic acid sequences that are expressed by human prostate cancer cells. The nucleic acid sequences or the encoded proteins are useful as targets for treating, preventing and/or diagnosing cancers, particularly prostate cancer. The present sequence is one such nucleic acid of the invention.
SOS	Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;
% # D	Query Match 93.0%; Score 1229; DB 14; Length 4839; Best Local Similarity 100.0%; Pred. No. 0; Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0
4d 8d	93 GGAAAGCTAGCGGCAGAGGCTCAGCCCCGGCGGCAGCCGCGCCCGCTGCCAGCCCATT 152
음 성:	153 TTCCGGACGCCACCCGCGGGACTGCCGACGCCCCCGGGGCTGCCGAGGGAAGGCCGGGG 212
8	13 GEGCGCAGCGGAGCGGCGCCCCGCGCAGCGCGCGCGGGAAACTTGGCGGCGCGCGC
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05-DEC-2001;
03-OCT-2002;
04-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel proteins and their coding sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-sequences). The proteins and their coding sequences are useful for treating a disease associated with NF-kappaB activation, such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New purified protein that activates nuclear factor kappa B (NF-kappaB), useful for treating inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases or ischemic disorders.
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               GGGCTGGGGCTGCGTAGGTGAAAAGGCAG 1321
                                                                  TCTGGAGCAAAGAATAAACAGAAAGGACACCTCTCTAGGGTCCCCAGGGGGGCC 1292
                                                                                                       CCTTGCTGGAGGGGACCCGGCTCCACCACACACACACCCGCCCCCTAGAGAGCGCAGCCA
                                                                                                                     CCTTGCTGGAGGGGACCCGGCTCCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCA
                                                                                                                                                            AGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGCAGTGGGCCGCCCT
                                                                                                                                                                          AGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCT
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RESULT 13 ADX97454 ID ADX97 XX

ADX97454

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                                                                                                                                                                                                                                                                               The invention relates to a novel human nucleic acid sequence of the pancreas and its encoded protein. The invention further comprises:

C proteins and peptides, preferably isolated, that contain a sequence concoded by the novel nucleic acid; and methods for diagnosis and content of pancreatic cancer, using a substance that inhibits or binds to the protein or its DNA, including: an antisense oligonucleotide, short correctly particularly having a malecular weight below 5000, conspand molecule, particularly having a molecular weight below 5000, conspand antibody, preferably human or humanized, that binds to the pancreatic DNA, an aptamer or consocional antibody, preferably human or humanized, that binds to the pancreatic DNA, an aptamer or consocional antibody, any of which may be derivatized with a reporter consocional antibody, any of which may be derivatized with a reporter consocional antibody, any of which may be derivatized with a reporter consocional antibody, and their encoding DNA have cytostatic compound, immunostimulant and/or radioisotope. The novel and/or expression of genes and their encoding DNA have cytostatic consocional pancreatic proteins associated with pancreatic consocional consocional proteins associated with pancreatic consocional consoc
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Best Local S
Matches 909
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P-PSDB; ADX97525.
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(SPEC/)
(LICH/)
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                                                                                                                                                                                                                                                                               Sequence
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Lichtner R,
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(PILA/)
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SPECHT T.
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TTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGATCACGTGC
                                       TCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG
                                                                                                                     ATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGGGCAGCCCAATGTC
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Staub E,
                                                                                                                                                                                                68.8%; Score 909; D
llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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vulnerary; gene therapy; vaccine; gene; ss
                                  retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting wound healing; contraception; cytostatic; cardiant; immunomodul
                                                                                                                  Human; differential expression; cancer; angiogenic disonibrotic disorder; psoriasis; ischaemia; heart disease; inflammatory disease; autoimmune disease;
                                                                                                                                                                                                                                  Cancer/angiogenesis/fibrosis-related nucleic acid,
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                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1321
                                        drug targeting;
nt; immunomodulatory;
                                                                                                                                                                                                                                     SEQ ID NO:127
                                                                                                                                                                              disorder;
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TCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG

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                                                                                                                 The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

CC whose expression is upregulated or downregulated in specific cancers or

CC other diseases such as angiogenic or fibrotic disorders, and to methods

CC of determining the presence or absence of a pathological cell in a

CC patient by detecting a nucleic acid at least 80% identical to those of

CC the invention or by detecting a polypeptide of the invention. The

CC invention also relates to expression vectors and host cells comprising a

CC nucleic acid of the invention; antibodies which specifically bind a

CC polypeptide of the invention; use of such antibodies for drug targeting;

CC and methods of screening for modulators of activity or expression of the

CC polypeptides and mucleic acids. The nucleic acids, polypeptides,

CC antibodies and methods are useful for diagnosing, prognosing and treating

CC cancer and other conditions such as psoriasis, ischaemia, heart disease,

CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal

CC cancer so the invention such as psoriasis, ischaemia, heart disease,

CC atherosclaristation syndromes, scarring and uterine fibroids. They may

CC also be useful in wound healing and in contraception. The present

CC sequence represents a nucleic acid sequence of the invention.
                                  Matches
                                                             Query Match
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08-FEB-2002;

13-FEB-2002;

20-FEB-2002;

29-MAR-2002;

04-AAR-2002;

12-APR-2002;

16-JUN-2002;

16-JUN-2002;
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14-DEC-2001;
08-JAN-2002;
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29-NOV-2001;
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                                                                                             Sequence
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                                 864;
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                                                                                             864
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   ATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGCCGGGCAGCCCAATGTC
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2002US-034734JP.
2002US-0355250P.
2002US-03550714P.
2002US-0359077P.
2002US-036809P.
2002US-0370110P.
2002US-0370214P.
2002US-0386614P.
2002US-03977246P.
2002US-0397775P.
2002US-0397775P.
2002US-0397845P.
2002US-0397845P.
                                  Conservative
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2001US-0334393P.
2001US-0335394P.
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R, Watson SR,
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                                                                                              Prostate cancer; prostate
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GCCAGGGGCGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA

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279 701 219

339 761 TGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA TGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA

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CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGATGGTGATGGTGGTGGTGG

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CGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGG

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ATCCGTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGG

ATCCGTACCTGCAGCACGAGATCGACCTGCCACCCATCTCGCTGTCAGACGGGGAGG

459 881 399 821

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Query Match
Best Local S
Matches 800
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08-DEC-2000;
08-DEC-2000;
08-DEC-2001;
24-JAN-2001;
16-MAR-2001;
                                                                                                              from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancerassociated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications. ABK92115.ABK92263 represent prostate cancer-associated polynucleotide
                                                                                                                                                                                                                                                      The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived expressed in prostate tumour tissue or in prostate cancer and are derived
                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a prostate cancer-associated transcript in a cell in a pauseful for diagnosing prostate cancer (PC) or screening modulators by determining if prostate cancer-associated genes are expressed in prostate tissue.
                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Claim
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P-PSDB; ABG61805.
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06-APR-2001;
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 al Similarity
800; Conserv
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2000US-00733742.

2001US-02639579.

2001US-0276791P.

2001US-0276888P.

2001US-0286214P.

2001US-0286214P.

2001US-0286214P.

2001US-028629P.
 60.6%; Score 800; llarity 100.0%; Pred. No. Conservative 0; Mismatch
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                                                                      BP;
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Novel isolated androgen-regulated gene designated as
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31-JAN-2000;
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2000US-0179045P.
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/product= "Human PMEPA1 protein"
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                                                                                                                                                                                                                                                                       Polynucleotide array, useful for diagnosing or prognosing prostate cancer, comprises a planar, non-porous solid support and a set of polynucleotide probes attached to the solid support.
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26-JAN-2001; 2001US-00769482.
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                                                                                                       Similarity
            TGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA 641
                                                           CGGAGCTGGAGTTTGTTCAGATCATCATCATCCTGGTGGTGATGATGGTGATGGTGGTGG 581
TGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA
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                                                                                                                      Androgen-regulated gene; ARG; PMEPA1; prostate cancer; CaP; prostate-related disease; gene therapy; vaccine; human; gene;
                                                                                                                                                           Human PMEPA1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-2000;
31-JAN-2000;
26-JAN-2001;
18-MAR-2003;
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DB; ADO39828.
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22-AUG-2001;
25-SEP-2001;
12-DEC-2001;
05-MAR-2002;
The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal
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Hoersh S,
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02-JAN-2002;
03-APR-2002;
                                                                                                                                                                                                                                                                             ACC49493 to ACC49552 encode the human tumour-associated antigenic target (TAT) proteins given in ABP97175 to ABP97234. The present invention describes an isolated antibody that binds to a polypeptide having at least 80 % sequence identity to any of the 60 150-800 residue amino acid sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking its associated signal peptide, encoded by any of the 60 2000-3000 base pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have cytostatic activity. The antibody can be used for treating or diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast cancer, colon cancer; oversian cancer, prostate adenocarcinomas, renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibodies against tumor-associated antigenic target polypeptide useful for treating or diagnosing tumors or cancers in mammals, e.g. prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
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28-MAR-2001; 2001US-00821812.
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                     The present invention relates to a androgen regulated prostate specific polypeptide-5 (ARP-5) and its encoding nucleic acid. The invention is useful for diagnosing and treating prostate cancer or other prostate pathologies such as benign prostatic hyperplasia or prostatitis. The invention is also useful in gene therapy. The present sequence is the
                                                                                                                                                                                                                                                             New androgen regulated prostate specific polypeptides (e.g. ARP-5, -3 -4) and encoding nucleic acids for diagnosing, preventing or treating prostate cancer or other prostate pathologies (e.g. benign prostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAR-2001;
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                                                                                                                          cc individual having contracted cancer, which comprises determining the cc microsatellite status of the tumor. The microsatellite status or the cc microsatellite status of the tumor. The microsatellite status or the cancer is determined by a method cc comprising; (a) obtaining a sample from the individual having contracted cc and/or amount of which forms a pattern that is indicative of the cancer; the sample comprising gene expression products, the presence cc microsatellite status or the hereditary or sporadic nature of the cancer; (b) determining the pattern, and obtaining an indication of the gene expression comproducts forming a pattern used to determine the cancer in the individual based on step (b). At least one or two of the gene expression products forming a pattern used to determine the cancer cc microsatellite status or the hereditary or sporadic nature of the cancer in the individual based on step (b). At least one or two of the gene expression products forming a pattern used to determine the cancer cc microsatellite status or the hereditary or sporadic nature of the cancer cc microsatellite status or the hereditary or sporadic nature of the cancer cc are selected individually from any of the 134 genes comprising 367-7850 bp (AEB22706 to AEB22839), given in the specification. Also included are: creating a classified cancer, comprising at least one malignancy of a cell; a method for treating a hidridual; a method for reducing malignancy of creating a classified cancer, comprising at least one marker in an individual having contracted cancer, cc comprising at least one marker in an individual having contracted cancer, cc comprising at least one marker one marker in a sample determining the prognostic marker, where the microsatellite status and the prognostic marker is determined simultaneously or sequentially. The method above is useful for probacing an assay contracted composition for the treatment of a cancer in animal tissue. The method is useful for probacing an adenocarcinoma. a carcinoma.
                                                              Query Match
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immune disorder; neoplasm; colon tumor; gastrointestinal disease;
adenocarcinoma; carcinoma; screening; diagnostic; prognostic;
pharmaceutical; ds; gene.
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CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGG
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                                                                                                                                                                           a sarcoma,
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; 2004DK-00000096.
; 2004DK-00000586.
; 2004DK-00001843.
                                                               Conservative
                                                                                                                                                        colon cancer, e.g. an adenocarcinoma, a carcinoma, sarcoma, and/or a lymphoma. The present sequence rej-associated gene used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jensen
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                                                                                                                            1088 A; 1150 C;
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                                                                            Score 800;
Pred. No.
                                                               Mismatches
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                   WO2005064009-A1
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cancer; genetic marker; lymphoma; cytostatic; hematological disease;
immune disorder; neoplasm; colon tumor; gastrointestinal disease;
adenocarcinoma; carcinoma; screening; diagnostic; prognostic;
Homo sapiens
                                         pharmaceutical;
                                                                                                                                                 Human colon
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                                                                                                                                                                                                                                                                          AEB22832 standard; DNA; 4538
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                                                                                                                                            cancer-associated gene SEQ ID NO:127
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CC microgatellitte status or the hereditary or sporadic nature of the cancer; CC (b) determining the presence and/or amount of the gene expression CC products forming the pattern, and obtaining an indication of the CC microsatellite status or the hereditary or sporadic nature of the cancer CC in the individual based on step (b). At least one or two of the gene CC expression products forming a pattern used to determine the CC are selected individually from any of the 134 genes comprising 367-7850 (c) p(ABB22706 to ABB22839), given in the specification. Also included are: CC are selected for producing antibodies against an expression product of a cell; a method for producing antibodies against an expression product CC of a cell; a method for producing antibodies against an expression product CC of a cell; a method for reducing an individual; a method for reducing malignancy of CC action of cancer, comprising at least one macleic acid and/or probe; and an assay, comparising at least one marker capable of determining the microsatellite status in a sample and at least one marker in a sample determining the microsatellite status in a sample and at least one marker in a sample determining the composition for the treatment of a cancer in an individual. The method above is useful for producing an assay for classifying cancer in animal tissue. The present set of composition for the treatment of a cancer in an individual having contracted cancer, i.e. colon cancer, e.g. an adenocarcinoma, a carcinoma, a sarcoma, and/or a lymphoma. The present sequence represents a concertion of the treatment of a cancer in an individual having contracted cancer.
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Best Local Similarity
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24-JAN-2004;
07-APR-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of classifying the cancer in an individual having contracted cancer, which comprises determining the microsatellite status of the tumor. The microsatellite status or the hereditary or sporadic nature of the cancer is determined by a method comprising: (a) obtaining a sample from the individual having contracted
                                                                                                                                                                                                                                                                        Sequence 4538 BP; 1090 A; 1151 C; 1179 G; 1118 T; 0 U; 0 Other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer, the sample comprising gene expression products, the presence and/or amount of which forms a pattern that is indicative of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                               GCCAGGGGCGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA
                                                                                                        TGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA
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                                                                                                                                                                    CGGAGCTGGAGTTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGATGGTGGTGGT
   GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG
                                                                                          TGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA
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; 2004DK-00000096.
; 2004DK-00000586.
; 2004DK-00001843.
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                                                                                                                                                                                                                             Score 800;
Pred. No.
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RESULT 25
AAI57868
ID AAI5
                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI57868
                  21-JAN-2000;
25-APR-2000;
                                                    23-DEC-1999;
                                                                                     26-DEC-2000;
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                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polymeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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Zhou
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sded polypeptides (AAM38642-AAM42213) with nootropic,
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Wang Z,
Goodrich
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AGTCGGTGCGCGCACCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCA
                                                 ACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGG
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; 2000US-00653450.
; 2000US-00662191.
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RESULT 26
ADP17545
ID ADP177
XX ADP1
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                                                                                                                                                                                                                               New PMEPAl polypeptide, useful in inhibiting the growth of a prostate cancer cell, diagnosing or prognosing prostate cancer, evaluating the efficacy of a treatment in a patient with prostate cancer or in gene
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The present sequence encodes the human androgen regulated PMEPA1 protein (I), which inhibits the growth of prostate cancer (LNCaP) cells in a colony-forming assay. Also described: (1) a method of reducing the

androgen receptor in a prostate

cancer

(2) a

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31-JAN-2000;
26-JAN-2001;
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                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                              The present invention relates to the identification and characterisation of a novel androgen-regulated genes (ARGs) that exhibits abundant expression in prostate tissue. The novel gene is designated PMEPA1. The invention is useful for diagnosing and prognosing prostate cancer. The invention is also useful in hormonal therapy. The present sequence is human PMEPA1 coding cDNA. The PMEPA1 gene is located on chromosome 20q13
                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; SEQ ID NO 2;
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                                                                                                                                               28-JAN-2000;
31-JAN-2000;
26-JAN-2001;
                     Srivastava S,
                                                          (SRIV/)
(MOUL/)
(XULL/)
                                                                                                                                                                                                                             09-MAY-2003; 2003US-00434479
                                                                                                                                                                                                                                                                 13-MAY-2004.
                                                                                                                                                                                                                                                                                                      US2004092469-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Androgen-regulated gene; ARG; PMEPA1; prostate cancer; CaP; prostate-related disease; gene therapy; vaccine; human; gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PMEPA1
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; 2000US-0179045P.
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; 2003US-00390045.
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WPI; 2004-374986/35
P-PSDB; ADO39828.
GENBANK; AF224278.
                            New PMEPA1 polypeptide that inhibits the growth of LN prostate cancer (LNCaP) cells in a colony-forming assay, useful for detecting, preven
treating prostate cancer.
                                     preventing
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Claim 3; SEQ ID NO 2; 78pp; English.

The invention relates to androgen-regulated gene (ARG), PMEPA1 and its encoded protein. PMEPA1 polypeptide is useful in inhibiting the growth of a prostate cancer (Cap) cell. It is also useful for reducing the expression of an androgen receptor or modulating the expression of a androgen receptor or modulating the expression of a gene in a prostate cancer cell. PMEPA1 sequence is useful in gene therapy, useful to prepare vaccines, useful as markers of prostate cancer and other prostate-related diseases, and as targets for therapeutic intervention in prostate cancer and other prostate-related diseases. PMEPA1, its encoding nucleic acid or the antibodies are useful for detecting, preventing and treating prostate cancer. The present sequence is human PMEPA1 cDNA. This sequence is used in the exemplification of the invention. invention.

Sequence 759 BP; 152 P, 269 Ç 226 G; 112 T; 0 U; 0 Other;

Query M Best Lo Matches	Query Match 57.2%; Score 755; DB 12; Length 759; Best Local Similarity 100.0%; Pred. No. 0; Matches 755; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
. ¥	522 CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGATGATGATGGTGATGGTGGTGG 581	
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γ	642 GCCAGGGGGGAGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA 701	
8	125 GCCAGGGGCGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA 184	
¥	702 GCACAGTGTCAGGCAACGGAATCCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG 761	
ъ	185 GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG 244	
Ϋ́	762 ACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCT 821	
Ъ	245 ACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCT 304	
Ϋ́	822 ATCCGTACCTGCAGCAGGAGATCGACCTGCCACCCATCTCGCTGTCAGACGGGGAGG 881	
Ъ	305 ATCCGTACCTGCAGCACGAGATCGACCTGCCACCATCTCGCTGTCAGACGGGGAGG 364	
Ŋ	882 AGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCCGAGCAGCAGCAGCTGG 941	
ъ	365 AGCCCCCACCCTACCAGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGG 424	
Ş	942 AACTGAACCGGGAGTCGGTGCGCGCACCCCCCAAACAGAACCGTCTTCGACAGTGACCTGA 1001	
do	425 AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 484	
Ş	1002 TGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCGCCA 1061	
ъ	485 TGGATAGTGCCAGGCTGGGCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCGCCA 544	
Ŋ	1062 CGTGCTACGGCAGCGGGGGGGCGATGGAGGGGCCCGCCCCCCCC	
8	545 CGTGCTACGGCAGCGGGGCGCATGGAGGGGCCGCCCACCTACAGCGAGGTCATCG 604	
Ŋ	1122 GCCACTACCCGGGGTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGG 1181	
₽	605 GCCACTACCCGGGGTCCTTCCAGCACCAGCAGCAGTGGGCCGCCCTCCTTGCTGG 664	

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ARASULT 29
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The present sequence encodes a human TANGO 261 polypeptide. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factorassociated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder;
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                                                                                                                                                                                                                                                                            Claim 2;
                                                                                                                                                                                                                                                                                                                                           Novel human and murine secreted proteins 266 and 267 useful as modulating agents o
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                                                                                                                                                                                                                                                                            Fig 5; 175pp; English
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99.9%;
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                                                                                    Human neuron-associated proteins (NEUAP) can be used for for treating or preventing a disorder associated with decreased expression or activity of NEUAP. Antagonists of NEUAP are useful for treating or preventing disorder associated with increased expression or activity of NEUAP. NEUAP or their fragments or derivatives are useful for treating neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia and Parkinson's disease. NEUAPB are also useful for treating other demyelinating diseases, bacterial and viral meningitis, prion diseases including kuru, Creutzfeldt-Jakob disease, nutritional and metabolic diseases of the nervous system, neurofibromatosis, other developmental disorders of the central nervous system, cerebral palsy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              muscular dystrophy; central nervous system; CNS; peripheral nervous system; PNS; myopathy; schizophrenia; peripheral nervous system; PNS; myopathy; schizophrenia; actinic keratosis; arteriosclerosis; attherosclerosis; bursitis; cirrhosis; hepatitis; mixed connective tissue disease; MCTD; myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer; autoimmune disease; inflammation; acquired immunodeficiency syndrome; alboring; Addison's disease; adult respiratory distress syndrome; allergy; ankylosing spondylitis; amyloidosis; anaemia; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ischemic cerebrovascular disease; stroke; cerebral neopiasm; Alzheimer's disease; Pick's disease; Huntington's disease; dementia; Parkinson's disease; demyelinating disease; meningitis; prion disease; kuru; Creutzfeldt-Jakob disease; neurofibromatosis; cerebral palsy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human neuron-associated proteins and polynucleotides encoding thuseful for diagnosis, treatment and prevention of cell proliferative disorders including cancer, neuronal and neurological disorders.
                          neuroskeletal disorders, autonomic nervous system disorders, onerve disorders, spinal cord diseases, muscular dystrophy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 136; 145pp; English.
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Azimzai Y;
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                                                                   cranial
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metabolic, endocrine, and toxic myopathies, mental disorders including mood, anxiety and schizophrenic disorders, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD) myelofibrosis, paroxysmal nocturnal haemoglobinuria, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, and an autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, Werner syndrome, complications of cancer, hemodialysis, and extraorporeal circulation, viral, bacterial, fungal parasitic, protozoal, and helminthic infections, and trauma. This sequence was given the Incyte ID
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Sequence 1061 BP; 225 A; 342 Ç 326 168 T;

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Similarity

Ş S Ś В S 문 Ş 밁 밁 8 밁 Ś 문 δ 밁 S 문 Ş 밁 ð В 밁 밁 S 吊 δ Matches 1182 1122 1062 1002 705 645 585 525 465 405 345 642 582 522 825 765 942 882 822 762 285 702 225 165 799; CGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGGT GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG GCCAGGGGCGGAGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA TGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA AAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGGCCGGGCTGGGG CGTGCTACGGCAGCGGCGGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCG TGGATAGTGCCAGGCTGGGCGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCA AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA AGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGG ATCCGTACCTGCAGCACGAGATCGACCTGCCGCCCACCATCTCGCTGTCAGACGGGGAGG ATCCGTACCTGCAGCACGAGATCGACCTGCCACCATCTCGCTGTCAGACGGGGAGG ACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCT ACCGCCTGGCCGTGCCGCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCT GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG GCCAGGGGGGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA TGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA CGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGG GCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGTGGGCCGCCCCCCCTCCTTGCTGG CGTGCTACGGCAGCGGCGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCG AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA AGCCCCCACCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGG **AAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCGGGCTGGGG** AGGGGACCCGGCTCCACCACACACACACCCCCCCCCTAGAGAGCGCAGCCATCTGGAGCA TGGATAGTGCCAGGCTGGGCGCCCCTGCCCCCCCAGCAGTAACTCGGGCATCAGCGCCA Conservative 56.7%; 99.9%; Score 749; DB Pred. No. 0; 0; Mismatches 0, 1; 0, Gaps 1301 1241 1181 1121 1061 1001 884 824 644 584 524 941 464 881 404 821 344 761 284 701 224 641 164 764 704 0

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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1085 BP;
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useful for treating inflammation, autoimmune diseases, cancers,
infectious diseases, bone diseases, AIDS, neurodegenerative dis
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DB; ADC37325.
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                                                                              GCCAGGGGCGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA
                                                                                                                                                          TGATCACGTGCCTGACCACCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA
                                                                                                                                                                                                                                                  CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGG
    GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG
                                                                                                                                                                                                                           CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGGTGG
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2001US-0335829P.
2002JP-00291302.
2002US-0415769P.
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RESULT 32 ABZ36103 ID ABZ36

ABZ36103 standard; cDNA; 1334 ВP

10-FEB-2003 (first entry)

Human secretory polynucleotide SPTM SEQ ID NO 267.

asthma; Crohn's disease; neurological disorder; epilepsy; cancer; Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease; multiple sclerosis; Parkinson's disease; cell proliferative disorder; anti-inflammatory; immunosuppressive; neuroprotective; nootropic; neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic; antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus; secretory polynucleotide; secretory protein; gene; ss Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;

Homo sapiens.

WO200283876-A2

27-MAR-2002; 2002WO-US009921

29-MAR-2001; 29-MAR-2001; 2001US-0280067P. 2001US-0280068P.

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                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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17-MAY-2001;
17-MAY-2001;
19-JUN-2001;
20-JUN-2001;
20-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human secretory proteins and polynucleotides, useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell proliferations or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-075543/07.
P-PSDB; ABP75660.
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Dufour GE, Hillman JL, Yu JY,
Daughtery SC, Dam TC, Liu TF,
Peralta CH, David MH, Lewis SA
Flores V, Marwaha R, Lo A, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
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                ATCCGTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGG
                                                                             ACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCT
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; 2001US-0291849P.
; 2001US-0299428P.
; 2001US-0299776P.
; 2001US-0300001P.
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99.9%;
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Pred. No. 0;
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Tuason O, Yap PE, A
Nguyen DA, Kleefeld
Nguyen AJ, Panzer SR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TANGO 266; TANGO 261; TANGO 261; TANGO 267; TANGO 267; Cellular proliferation; cellular differentiation; cellular adhesion; cellular broliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchital asthma; bronchiectasis; intestinal disorder; speen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflamation; meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-2001
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                                                                                                              01-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder;
  Barnes
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                                                        (MILL-) MILLENNIUM PHARM INC
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                                                                                                                                                                                                                                                                                                                                              /product= "TANGO 261"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC AAA75163-65 encode human TANGO 261 proteins. The specification also CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO CC polypeptides can be used to modulate cellular proliferation, modulate cellular adhesion. The proteins CC can be used to treat any von willebrand factor-associated disorder, CC trafficking and/or migration, modulate cellular adhesion. The proteins CC cellular adhesion in proliferative disorders, such as cancer, modulate the proliferation of cellular interactions, modulate cellular interactions modulate the proliferation, differentiation, and/or function of cells that appear in CC thematopoietic associated diseases and disorders, such as cancer modulate the bone marrow, and leukocytes, treat bone marrow, blood and pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, complete associated diseases, modulate the proliferation, differentiation, and/or cartilage cells and to treat bone and/or cartilage cells and to treat diseases, maltiple sclerosis, and cerebral coedema, bacterial and viral conceptabilitis, all treat hepatic diseases, brain cancers, hydrocephalus, brain conceptabilitis, and treat hepatic disorders. note: the present sequence codes not appear in the specification; it was created using information
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Best Local :
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19-OCT-2001;
07-NOV-2001;
20-NOV-2001;
02-JAN-2002;
                                                                                                                                                                                            New antibodies against tumor-associated antigenic target polypeptide useful for treating or diagnosing tumors or cancers in mammals, e.g. prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
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P-PSDB; ABP97219.
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                                                                                                                             Claim 2;
                                                                                                                                                                           carcinomas.
                                                                                                                                                                                                                                                                                                                                                                  Williams
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GENENTECH INC
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2001US-0331906P.
2002US-0345444P.
2002US-0369724P.
2002US-0369724P.
              ACC49552 encode the human tumour-associated antigenic target ins given in ABP97175 to ABP97234. The present invention in isolated antibody that binds to a polypeptide having at sequence identity to any of the 60 150-800 residue amino acid
                                                                                                                             45;
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Thang Z;
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Query Match
Best Local S
Matches 763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking lassociated signal peptide, encoded by any of the 60 2000-3000 base pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have cytostatic activity. The antibody can be used for treating or diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
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                      AAGAGAAAGGATAAACAGAAAAGGACACCCTCTCTAGGGTCCCCCAG 1285
                                                                                                          GCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGG 1181
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AAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAG
                                                                                                                                                                        GCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGTGGGCCGCCCTCCTTGCTGG
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RESULT 35 AAA75164

AAA75164 standard;

CDNA;

969

Query Match 52. Best Local Similarity 99. Matches 798; Conservative

52.8**%**;

0;

Score 698; DB 3; Pred. No. 7e-302; 0; Mismatches

Length 969 0

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Other;

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TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; halzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
                                                                                                                                                                                                                                                                         Novel human and murine secreted proteins designated TANGO 216, 261, 262 266 and 267 useful as modulating agents of cellular processes, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2000; 2000WO-US005226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA clone
                                                                                                                                                                                                                                              Disclosure; Page; 175pp; English.
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RESULT 36
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TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
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                                                                                                              cDNA clone
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129 641 69

CGGAGCTGGAGTTTCATCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGG

Matches

Conservative

0

Score 698; DB Pred. No. 7e-3 0; Mismatches

698; DB 3; No. 7e-302;

0

Gaps

0

522 10

Query Match Best Local Similarity

52.8%; A; 317

Sequence

969

B₽;

210

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294 G; 148 T; 0

U; 0 Other; Length 969 Indels

provided

disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders, note: the present sequence does not appear in the specification; it was created using information

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CC describes TANGO 266, TANGO 261 proteins. The specification also CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO CC cellular differentiation and/or modulate cellular proliferation, modulate cellular describes on the proteins CC can be used to treat any von Willebrand factor-associated disorder. CC regulate extracellular matrix structuring, cellular adhesion, and cell ctrafficking and/or migration, modulate cellular adhesion, and cell cellular describes, modulate cellular interactions, modulate cellular adhesion, and cell cellular describes, modulate the cellular interactions, modulate the cellular cancer, modulate the proliferation, and/or function of cells that appear in the bone matrow, and leukocytens, and/or function of cells that appear in the bone matrow, and leukocytens, treat bone marrow, blood and cellular congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and composition or oedema, emphysema, chronic bronchitis, bronchial asthma and compositis can disease, modulate the proliferation, differentiation, and/or cellular diseases, modulate the proliferation, differentiation, and/or cartilage cells and to treat diseases.

CC associated with the ovaries, and cerebral oedema, hydrocephalus, brain cerebral toxoplasmosis, Parkinson's cellular disease, cerebral toxoplasmosis, Parkinson's cellular cancers. bydrocephalus and celebrate collabates. Brain cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human and murine secreted proteins designated TANGO 216, 261, 266 and 267 useful as modulating agents of cellular processes, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1999;
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                                                                                                                                                                                                                                                                                             Human; ss; prostate specific nucleic acid; PSNA; prostate cytostatic; non-cancerous prostate disease; PSP; vaccine; prostate specific protein; metastasis.
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                              2000US-0244782P
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(DIAD-) DIADEXUS INC
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Recipon H, Chen ß Liu

New polypeptide useful for diagnosing and monitoring the presence and metastases of prostate cancer in a patient and as a component in databases for search analysis as well as in sequence analysis algorithms.

Claim 1; Page 166-167; 242pp; English.

The invention relates to an isolated polypeptide comprising a sequence with 60 % identity to one of prostate specific protein (PSP) sequences, cc or comprising an amino acid sequence encoded by one of 136 nucleotide cc prostate specific nucleic acids sequences, PSNA, (or a sequence that cc hybridises to it or is 60% identical to it), given in the specification. CC Also included are a vector comprising the polynucleotide, a host cell cc mystising the vector, an antibody specific for the PSP proteins and a cc vaccine comprising the protein or polynucleotide. The PSP and PSNA are cuseful for diagnosing and monitoring the presence and metastases of creative presence of prostate specific protein in a sample. An antibody to the PSP is useful for determining the presence of prostate specific protein in a sample, and for treating a cc patient with prostate cancer, which induces an immune response against creative prostate cancer cell expressing the nucleic acid or polypeptide and a component of the probes to detect, characterise and quantify hybridising nucleic acids from both genomic and transcript cand psnA are useful as components in databases for search analysis as components in databases for search analysis as components in databases for search nalysis as components in databases for search analysis as the protein and protein

Sequence 1583 BP; 361 A; 469 C; 457 G; 296 T; 0 U; 0 Other;

S 닭 8 밁 S 밁 8 맑 8 밁 S 맑 S 밁 S 밁 Ş Matches Query Match Best Local Similarity 1210 1247 1150 1187 1090 1127 1030 1067 1007 970 887 827 910 947 850 560; GCCACCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCAC GCGGGAGCGCTTCCACCGTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCT CGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAAGGATAAACAGAAAGGACACCC 1269 CCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGCGGCGCATGGA CCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACC GCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCAC GCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCT GCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCGCCTTGGCCGTGCCGCCCTTCGCCCA GCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCA GGGGCCGCCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCA GGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCA CCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGCGCATGGA CCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTG CCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTG CCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACC Conservative 100.0%; 42.4%; 0; Score 560; Pred. No. Mismatches 3.7e-240; DB 6; 0 Length 1583; Indels 0; Gaps 1209 1246 1149 1186 1089 1126 1066 969 1006 909 946 849 988 0

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RESULT 38
ADO00336/c
ID ADO00336 f
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17-JAN-2003
17-JAN-2003
17-JAN-2003;

18-APR-2003;

18-APR-2003;

18-APR-2003;

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18-APR-2003;

02-MAY-2003;

02-MAY-2003;

02-MAY-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunomodulator; antibacterial; virucide; antipsoriatic; cytostati
gene therapy; vaccine; inflammatory; CNS; immune disorder; cancer;
psoriasis; diabetes; early aging; hormonal imbalance;
ischemic heart disease; ulcerative colitis.
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15-NOV-2002
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2002US-0430645P
2002US-0430657P
2002US-0430668P
2002US-0430668P
2002US-043093P
2002US-043093P
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2002US-04333500P
2002US-0433350P
2002US-0433316P
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2002US-0433316P
2002US-0433116P
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2003US-0463708P
2003US-0463700P
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2002US-0422177P.
2002US-0422178P.
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2002US-0429302P
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2002US-0426430P
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2002US-0426384P.
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2002US-0421552P.
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14-JUL-2003;
14-JUL-2003;
15-JUL-2003;
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19-MAY-2003
22-MAY-2003
22-MAY-2003
29-JUN-2003
09-JUN-2003
09-JUN-2003
09-JUN-2003
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Halenbeck RF,
Wong JGP, Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-2003;
08-AUG-2003;
                                                                                                                                                                                                                                                                                                                                              The invention relates to a nucleic acid molecule comprising a polynucleotide sequence or its complement that encodes a polypeptide. nucleic acid is useful in preparing a composition for treating or preventing inflammatory, CNS, immune, bacterial or viral disorder, cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic heart disease or ulcerative colitis. This sequence corresponds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecules, useful in preparing a composition for treating or preventing e.g. inflammatory, CNS, bacterial or viral disorders, cancer, psoriasis, diabetes, ischemic heart disease or
                                                                                                                                                                                                                                                                                                                                    cancer, psoriasis, diabetes, early aging, heart disease or ulcerative colitis. This nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ulcerative colitis.
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P-PSDB; ADN99551.
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                                        GGGCGCCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCAGCTCCCGGCCCCGGCC
                                                                             GGGCGCCTCCCCCCGCCGCGCGCCTCCTGCATCCGGGGCCCCAGCTCCGGGGCGCCGGCC
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f, Kothakota s
~ Zhang F
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2003US-0485213P
2003US-048523P
2003US-0485223P
2003US-0485325P
2003US-0485355P
2003US-048646P
2003US-0486480P
2003US-0486891P
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2003US-048691P
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2003US-0493377P
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2003US-0472430P.
2003US-0476609P.
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Zeng C;
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Pred. No. 1.3e-17;
0; Mismatches 0,
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RESULT 39
ADN98767/c
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ID 9877/7/C
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PR 25-0C1
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immunomodulator; antibacterial; virucide; antipsoriatic; cycostatic;
gene therapy; vaccine; inflammatory; CNS; immune disorder; cancer;
psoriasis; diabetes; early aging; hormonal imbalance;
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2002US-0426394P.
2002US-0426394P.
2002US-042691P.
2002US-042691P.
2002US-0429326P.
2002US-0439651P.
2002US-0439651P.
2002US-0439651P.
2002US-0439668P.
2002US-0430668P.
2002US-0430668P.
2002US-0430684P.
2002US-0433937P.
2002US-0433937P.
2002US-04333316P.
2002US-04333316P.
2002US-04333316P.
2002US-0433730P.
2003US-0463700P.
2003US-0467201P.
2003US-0467201P.
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Best Local Similarity
Matches 409; Conserv
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19-MAY-2003;
19-MAY-2003;
22-MAY-2003;
22-MAY-2003;
22-MAY-2003;
09-JUN-2003;
09-JUN-2003;
09-JUL-2003;
09-JUL-2003;
08-JUL-2003;
08-JUL-2003;
08-JUL-2003;
14-JUL-2003;
18-AUG-2003;
08-AUG-2003;
08-AUG-2003;
08-AUG-2003;
                                                                                                                                                                                                                                                                                                                 The invention relates to a nucleic acid molecule comprising a polynucleotide sequence or its complement that encodes a polypeptide. nucleic acid is useful in preparing a composition for treating or preventing inflammatory, CNS, immune, bacterial or viral disorder, cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic heart disease or ulcerative colitis. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecules, useful in preparing a composition for treating or preventing e.g. inflammatory, CNS, bacterial or viral disorders, cancer, psoriasis, diabetes, ischemic heart disease or ulcerative colitis.
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                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 367; 532pp; English.
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P-PSDB; ADN99551.
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                                                                                                                                                                                                                                                                                   711 BP;
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  GGGCGCCTCCCCCGCGCGCGCGCCTCCTGCATGCGGGGCCCCAGCTCCGGGCGCCCGGCC
                                                                               CCGCGCACTGAGCCCCGGGCGCCCCCGGGGAACTTGGCCGGCGACCCCGAGCCCGGCGAGCCG
                                                                                                                                  TCAGCCCCGGCAGCGCGCGCCCCGCTGCCAGCCCATTTTCCGGACGCCACCCGCGG
                              GGGCGCCTCCCCCGCGCGCGCCTCCTGCATGCGGGGCCCCAGCTCCGGGCGCCGGCC
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2003US-0476621P.
2003US-0476632P.
2003US-0485218P.
2003US-0485218P.
2003US-0485223P.
2003US-0485223P.
2003US-0485223P.
2003US-0485235P.
2003US-0485325P.
2003US-048636P.
2003US-0486480P.
2003US-0486480P.
2003US-0486480P.
2003US-048649373P.
2003US-04893577P.
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2003US-0471306P.
2003US-0471336P.
2003US-0472420P.
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Kothakota S,
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Zeng
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Pred. No.
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Lin H, Linnemann
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nemann T,
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Pierce K,
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                                          The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and cantibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia,
                                                                                                                                                                                                                                                                                                              Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                           Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J;
Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lar
Kassam A, Crkenjakov R, Drmanac S, Dickson M, Labat I;
Leshkowitiz D, Kita D, Garcia V, Jones LW, Strache-Crain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR )
(HYSE-)
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02-JUL-1999;
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breast cancer; lun
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                                                                                                                                                                                                                                                                                  Claim 9; Page 793; 1046pp;
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99US-0142311P.
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                                                                                                                                                                                                                                                                                  English.
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583 GATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAG

Query Match
Best Local Similarity
Matches 401; Conserv

Conservative

0,

Mismatches

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5.3e-169;

30.4%; Score 401; 100.0%; Pred. No.

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408 BP; 81

A; 159 C;

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U; 0 Other; Length 408 Indels

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The invention relates to 9672 polynucleotides (ACL53866-ACL63537) which are differentially expressed in colon cancer cells. The invention also relates to vectors and host cells comprising a differentially expressed polynucleotide of the invention; a method for detecting a cancerous cell by detection of a gene product of the polynucleotides; a method for inhibiting a cancerous phenotype of a cell by inhibiting a gene product of the polynucleotides; a method of treating an individual with cancer by administration of a method of treating an individual with cancer by administration of a modulator of a gene product of the polynucleotides; and an isolated antibody that specifically binds to a polypeptide encoded
                                                                                                                                                                                                                                                 New isolated polynucleotides, which are differentially expressed in colon cancer cell, useful for treating cancer, e.g. colon cancer, breast cancer, or pancreatic cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by one of the 9672 polynucleotides. The polynucleotides, polypeptides, antibodies, and methods are useful for the detection of cancerous cells; for the diagnosis, prognosis and management of cancer; for the identification of agents that modulate the phenotype of cancerous cells; for the identification of therapeutic targets for cancer chemotherapy; and for the treatment of cancer, especially colon cancer and metastanized.
                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                        WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID
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Pred. No. 5.3e-169;
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20-JUN-2000;
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03-ALG-2000;
14-SEP-2000;
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29-NOV-2000;
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                                               ACCCACCATCTCGCTGTCAGACGGGGGGGGGGCCCCCACCCTACCAGGGCCCCTGCACCCT
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                                                                                                                                                                                                                                                                                                                      CTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCC
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                                                                                                 GGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCC
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2000US-0052317.
2000US-00598042.
2000US-00620312.
2000US-00633450.
2000US-00632191.
2000US-00693036.
2000US-00693036.
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Wehrman T,
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Xu C,
ic RT;
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Pred. No. 6.7e-166;
0; Mismatches 5;
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Xue
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Yang Y,
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Zhang
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, Zhao QA;
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The present invention describes a method (M1) for determining a toxicological response to an agent, which comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity, and so determining the presence of a toxic response to the agent. Also described: (1) an array comprising one or more polynucleotides selected from the genes corresponding to the partial sequences given in ABZ82842
                                                                                                                               Determining a toxicological response to an agent, useful drugs, comprises comparing the expression profile of one toxic response genes to a reference gene expression profi
                                                                                                                                                                                                      Alen
                                                                                                                                                                                                                 Neft
                                                                                                                                                                                                                                                                                                                                                                                    Toxicologically relevant
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                                                                                                                                                                                                                                          (PHAS-)
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                                                                                              455pp;
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                                                                                                                                                                                                                  Adkins K,
                                                                                                                                                                                                                                                                                                                                                                                    gene; toxicological response; gene;
                                                                                              English.
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                                                                                                                                 of one or
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e or more human
file indicative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC to ABZ84764, or their fragments of at least 20 nucleotides, or homologues cc; and (2) determining if a gene putatively identified to be a toxic cresponse gene plays a role on toxic response pathways by determining the cxpression profile of the gene after exposure of cells or a human subject to a known toxic pharmaceutical or industrial agent, comprising; (a) cxposing cells to an agent or isolating cells from a human subject who cc was exposed to an agent; (b) obtaining the test gene expression profile cfor a putatively identified toxic response gene after exposure to a known cc profile to the expression profile of a gene with a similar function or cc comparing the test profile to the expression profile to the expression profile to the expression profile to the standard toxic compounds. The methods are useful for creposure to other known toxic compounds. The methods are useful for credicting and determining toxicological responses on a cellular, organ credicting and determining toxicological responses on a cellular, organ cor system level. The arrays comprising the human genes are useful for toxicological screening of drugs, pharmaceutical compounds and chemicals
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                                                                                                                   GGCTGGGCGGCCCTGCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCA
                                                                                                                                                         AGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCA
                                                                                                                                                                                    AGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCA
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                                                                            GGCTGGGCGCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCA
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Pred. No. 1.9e-152;
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ABK12143 standard; cDNA; 693 ВP

05-JUN-2002 (first entry)

Human MIVR-1 homologous sequence #1.

RESULT 44
ABK12143/c
ID ABK122
XX ABK12
XX ABK12
XX ABK12
XX ABK12
XX O5-JU
COT O5-JU Human; ss; MIVR-1; Mechanically Induced Vascular Receptor 1; cyt-cardiant; cerebroprotective; antiarteriosclerrotic; cardiac cell; anti-apoptotic; vascular endochelial cell; cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis; heart failure; cytostatic;

AI761441.1.

Homo sapiens

WO200216416-A2

28-FEB-2002

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AAZ52964
ID AAZ5
XX
AC AAZ5
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DT 14-N
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                                                                                RESULT 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule encoding a CC Mechanically Induced Vascular Receptor (MIVR) 1 polypeptide having cardiac cell anti-apoptotic activity and fragments of it provided they cardiac cell anti-apoptotic activity and fragments of it provided they cardiac cell anti-apoptotic activity and fragments of it provided they cardiac cell sexpression vectors, host cells, the MIVR-cc 1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule comprising MIVR-1, CC IEX-1, VUDP-1, BTG-2 and TIS-11d or its expression product, determining cc if the anti-apoptotic activity is modulated and thereby identifying a modulator. The cardiac cell anti-apoptotic molecules and nucleic acids of the invention are useful for treating, diagnosing and monitoring cc progression of such diseases and disorders as characterised by increased apoptotic cell-death of vascular endothelial cells e.g. cardiac chapper trophy, myocardial infarction, stroke, arteriosclerosis and heart cardiac are apoptotic hare homologous to the cDNA for human MIVR-1 and which
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
      14-MAR-2000
                              AAZ52964;
                                                       AAZ52964 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 693 BP; 101 A; 205 C; 237 G; 149 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 101; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid molecule encoding Mechanically Induced Vascular Receptor-1 polypeptide, useful for treating cardiovascular diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee RT,
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                                                                                                                                               GG 1186
                                                                                                                                                                                          ACTACCCGGGGTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGG
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(first entry)
                                                       CDNA; 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 302; DB 6; Logical Pred. No. 9.8e-125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 693;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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      RESULT 46
AAA41265
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AC AAA41
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AAA41265

AAA41265 standard;

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Query Match
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Matches 321; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 812 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human nucleic acid sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate tumor cDNA library derived EST fragment #107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in AAY73814-Y74252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 269-270; 502pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY74135, AAY74136, AAY74137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-621386/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE19820190-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pancreas; tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (META-) METAGEN GES GENOMFORSCHUNG MBH.
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CCCCACCCTACCAGGGCCCCTG
                                                                                  CGTACCTGCAGCACGAGATCGACCTGCCACCACCATCTCGCTGTCAGACGGGGAGGAGC 884
                                                                                                                                                            GCTGGCCGTGCCGCTTCGCCCAGCGGGGGGCTTCCACCGCTTCCAGCCCACCTATC
                                                                                                                                                                                                                    CAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACC
                                                                                                                                                                                                                                          CAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCC
                                                                                                                                                                                                                                                                                                                              AGGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGGACCA
                                                                                                                                                                                                                                                                                                                                                                                   TCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCC
                                                                                                                                                                                                                                                                                                                                                                                                          TCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCC
                                                                                                                                    GCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATC
                                                                                                                                                                                                                                                                                                     AGGGGCGGAGGAGAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCA
                                                        CGTACCTGCAGCACGAGATCGACCTGCCGCCCACCATCTCGCTGTCAGACGGGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.5%;
nilarity 99.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST; expressed sequence tag; human; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 271;
Pred. No. 7
                906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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7.2e-111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U; 0 Other;
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Human secreted 21-AUG-2000

expressed sequence tag SEQ ID

NO:5.

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(first entry)

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Matches 229
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Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                     the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the SESTS. Proteins encoded by the SESTS are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccautoimmune disorder; multiple sclerosis; allergic condition; autoimmune disorder; multiple sclerosis; allergic condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be used for gene therapy and in vaccines. The sESTs are useful as probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 180; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection; depression; psoriasis;
                                                                                                                                                                                                                                                                                                                            disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA43420 to AAA43425 represent linker variants which are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic;
haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial;
antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence tags (SESTs), isolated from human, mouse, xenopus and rat sources. The sESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated
                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEMY ) GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as autoimmune,
563 ATGATGGTGATGGTGGTGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGG
                                                                                                                                                                                                                                                                                             exemplification of the present invention
                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotides, and encoded proteins, comprising secreted sequence tags (sESTs), useful for treating various disorders and central nervous system disorders.
                                                                                                                                                                                                                                 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to AAA43419 represent specifically claimed secreted
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Treacy M;
                                                                                                                                                                                                                                 BP; 46 A; 85 C; 82 G; 41 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0104435P
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                                                                                              Score 229; DB Pred. No. 4.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The activities include: chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.
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                                                                                                    4.7e-92;
hes 0;
                                                                                                                                                                    DB 3;
                                                                                                                                                                 Length 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĘĄ,
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy; vaccine;
                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed
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RESULT 47
ADW43372
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Best Local
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                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel nucleic acid sequences that are expressed by human prostate cancer cells. The nucleic acid sequences of the encoded proteins are useful as targets for treating, preventing and/or diagnosing cancers, particularly prostate cancer. The present sequence is one such nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADW43372 standard; DNA; 310
                                                                                                                                                                                                                                                                                                                  Sequence 310 BP; 64 A; 75 C; 108 G; 63 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid sequence that is expressed by human prostate cancer cells, useful as target for treating, preventing and/or diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-057996/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-2003; 2003US-0482595P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUN-2004; 2004WO-IB002394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prostate cancer related gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADW43372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXON-) EXONHIT THERAPEUTICS
                                                                                                                                                                                                                                                         Local Similarity
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                               642
                                                                                                                  582
                                                                                                                                                        102
                                                                                                                                                                                                  522
                                                                                                                                                                                                                                      209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
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                                                                                                     TGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA
                                                                                                                                                        CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGGTGGTGG
                                                                                                                                                                               CGGAGCTGGAGTTTTGTTCAGATCATCATCATCCTGGTGGTGATGATGGTGATGGTGGTGG
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                                 GCCAGGGGGGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid sequence that is expressed by human prostate cancer cells, useful as target for treating, preventing and/or diagnos: cancers, particularly prostate cancer.
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Human; ss; sequencing by hybridisation; SBH; expressed genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 579 BP;
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                                      Human adult brain cDNA #2074.
                                                                13-OCT-2003
                                                                                                                ACH14862 standard; cDNA; 467
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Best Local Sim
Matches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
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(DICK/)
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 467 BP; 133 A; 121 C; 131 G; 74 T; 0 U; 8 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2074; 44pp; English.
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Web : www.genoscope.cns.rr) st strand cDNA was primed with a NotI-oligo(dT) primer. nd enriched, double-strand cDNA was digested with Not I	Genoscope.  Direct Submission  Submitted (20-UUL-2004) Genoscope - C Submitted (20-UUL-2004) Genoscope - C  BP 191 91006 EVRY cedex - FRANCE (B-m	Contact : Feng Liang Email : fliang@lifetech.com URL http:/fulllength.invitrogen.com/ InvitroGen Corporat Faraday Avenue 2 (bases 1 to 901)	1 (bases 1 to 901) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Impublished	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Euarchontoglires; Primates; Cata Hominidae; Homo.		890	901 bp mRNA linear HTG length cDNA clone CSODJ015YF12 of T cells (Jurkat 0-normalized of Homo sapiens (human).		ALIGNMENTS	A1752180 BQ133789	DN389076 BE457585	CF722779 BU981288	BW229990 CN368942	BF425160 AA792353	CG499617 DN348989 BY772109	CN4 02626	BY192028	BY176775	AI119251	BB841720	CG549167 BY147222	BY217229 BY220368	BY338273	BI818861	DN394778 CG549590	CF531239	BY353066	AV948856 CB153093	CN368930 CG512689
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/plasmid="pCMVSPORT_6"
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM.12791 row: n column: 06
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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AGENCOURT_6707077 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5754437
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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                    GGGCGGAGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACA
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                                                                                    ACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAG
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5754437"
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BQ641849
BQ641849.1 GI:21766021
EST.
                                                                                                                                                                                               Plate: LLCM2493 row: g column: High quality sequence stop: 571.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 967)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/tissue type="normal pigmented retinal epithelium" /lab host="NIH MGC_43" /clone_lib="NIH MGC_43" /clone_tib="NIH MGC_43" /clone_tib="NIH MGC_43" /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                             clone="IMAGE:6292265"
                                                                                                                                          'mol_type="mRNA"
'db_xref="taxon:9606"
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                                                                                                                                                                                                                                       DN992322 647 bp mRNA linear EST 17-MAY-20 TC124411 Human adult whole brain, large insert, pCMV expression library Homo sapiens cDNA clone TC124411 5' similar to Homo sapiet transmembrane, prostate androgen induced RNA (TMEPAI), transcript
                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 6
                                                                                                                                                                                           DN992322
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                                                                                                                                                                                                               variant 4, mRNA sequence.
                                                                                                                      Homo sapiens (human)
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Birkett, C., Cho, J.,

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High Throughput cDNA Cloning
OriGene Technologies, Inc. ( www.origene.com )
6 Taft Court, Suite 100, Rockville, MD 20850, 1
Tel: 301 340 3188
Fax: 301 340 8606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang,X., Jay,G. and He,W.
High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
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Tel: (301) 340-3188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OriGene Technologies, Inc.
6 Taft Ct. Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cDNA@origene.com
This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc.
Please contact Origene for access.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2005)
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Technologies Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.origene.com
Seq primer: pCMV6 5pri
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CCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCTATCCGTACCTGCAGCACG
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                                 CCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACG
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: Brain; Vector: pCMV6-XL5; Site 1: BcoR1; Site 2: Xhol/Sal1 compatible end ligatio; Oligo-dr primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random
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/clone_lib="Human adult whole brain, large insert,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 588; DB 8;
Pred. No. 2.2e-278;
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Query Match
Best Local Similarity
Matches 668; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 916)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ954555 916 bp mRNA linear AGENCOURT_8825282 Lupski_sciatic_nerve Homo sapiens IMAGE:6204609 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM13626 row: c column: 10 High quality sequence stop: 669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGG 959
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                                                                                                        5'-GACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size select 1 kb for average insert length 1.87 kb. This is a pr library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (College of Medicine) and is available through Life Technologies."
                                                                                                                                                                                                                          /clone lib="Lupski sciatic_nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                                                                                                                                                                                                          /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         'clone="IMAGE: 6204609"
                                                                                                                                                                                                                                                                                                                                                                                                                                             mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   sex="male"
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                      43.0%;
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Euarchontoglires; Primates; Catarrhini;
    Score 568; DB Pred. No. 1.6e 0; Mismatches
                         DB 5; I
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Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethqsda, MD 20892-2740, USA
                                                                                     Hominidae; Homo.

1 (bases 1 to 609)

Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A., Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.

Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.

Expressed sequence tag analysis of human retina for the leavest sequence tag analysis of human retina for the leavest sequence tag analysis of human retinal cDNA and splicing of other retina-preferred gene transcripts splicing of other retina-preferred gene transcripts will be sequenced. Vis. 8 (4), 196-204 (2002)
                                                                                                                                                                                                                                                                                                                                                           BQ636742 609 bp mRNA linear EST 15. hd13h06.y1 Human Retina cDNA (Un-normalized, unamplified): Homo sapiens cDNA clone hd13h06 5', mRNA sequence.
                                                      Mol. Viš. 8 (4), 1
12107411
Contact: Wistow G
                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                         Homo sapiens
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BQ636742.1 GI:21761201
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Plate: 13 row: h column: 06
Seg primer: M13RP1 reverse primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301 402 3452
Fax: 301 496 0078
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//dev_stage="Adult"
/lab_host="EMDH10B"
/lab_host="EMDH10B"
/clone lib="Human Retina cDNA (Un-normalized,
unamplIfied): hd/he"
/note="Organ: Eye; Vector: pspORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pspORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
Instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer-adapter [5'-pGACTAGTTCTAGATCGCGAGCGGCCC(T)15-3']. EST analysis performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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1 (bases 1 to 551)

1 (bases 1 to 551)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Melton,D., Brown,J., Kenty,G., Gradwohl,G., Clifton,S., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hiller,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Schmitt,A., Theising,B., Mitter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Claims,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MA 02138
Tel: 617-495-1812
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Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consortium, for clone orders contact: info@image.llnl.gov
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                                                                                                                                                                               /clone lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pspORT1; Site 1: Not 1;
Site 2: Sal 1; Starting library constructed using
Superscript Plasmid Library kit (Life Technologies) cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
                                                            plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
                                                         by hydroxyapatite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="Adult"
/lab_host="DH108"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
Contact: Kovacs, KF
Contact: Kovacs, KF
High Throughput cDNA Cloning
OriGene Technologies, Inc. ( www.origene.com )
6 Taft Court, Suite 100, Rockville, MD 20850,
Tel: 301 340 388
Fax: 301 340 8606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Н
                                                                                                                    Hominidae; Homo.

1 (bases 1 to 601)

1 (bases 1, Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L. Birkett, C., Cho, J., Gau, Y., Hamer, R., Sun, Z., Wong, J., Wu, M., Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M., Zhang, X., Jay, G. and He, W.

Zhang, X., Jay, G. and He, W.

High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                      DN991959 mRNA linear EST 17-MAY-2005 TC113706 Human adult whole brain, large insert, pCMV expression library Homo sapiens cDNA clone TC113206 5' similar to Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                       DN991959
DN991959.1 GI:66251790
EST.
                                                                                                                                                                                                                                                                                                                                                                                      variant 1, mRNA sequence.
                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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Technologies Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.origene.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cDNA@origene.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGCCGGCAGCCCAATGTCTCCTGCA 479
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/clone Tib="Human adult whole brain, large insert,
/cspression library"
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Pred. No. 1.1e-255;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rual, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O., Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C., Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics Genome Res. (2004) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert Length: 605 Std Brror: 45.00
Plate: 11020 row: 10 column: D
Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
High quality sequence start: 11
High quality sequence stop: 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, I
Tel: 617 632 5180
Fax: 617 632 5739
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Marc Vidal Laboratory
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Marc Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry c
results from a PCR reaction using an MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae; Homo.
1 (bases 1 to 605)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: ATGATGGTGATGGTGGTG
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                                                                                  GCACAGCCAGGGGGGGGGGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTC
                                                                                                              GCACAGCCAGGGGGGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTC
                                                                                                                                                                                                                      GGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCG
                         GGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCC
                                                                                                                                                                          GGTGGTGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCG
GGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCC
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 DONOR vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collection"
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/tissue_type="mixed"
/clone_lib="Full Length cDNA from the Mammalian Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
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Pred. No. 1e-252;
0; Mismatches
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C full-length cDNA as
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COMMENT
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AL558881 Homo sapiens Clone C
Homo sapiens cDNA clone C
AL558881 GI:46184268
                                                                                                                                                                                                                                                                                                                            Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 9167 EVRY cedex - FRANCE
Email: segrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand.cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                    For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODJ015DC06NP1&c=9945.r.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Feb 15, 2001 this sequence version replaced gi:31283014 Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 850)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR
                                                              /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMAI
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)
10-NORMALIZED"
                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODJ015YF12"
                                                                                                                                                                                                                                                   Location/Qualifiers
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Best Local Similarity 99.5%;
Matches 733; Conservative
                                                                ORGANISM
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                                                                                                     BQ575741 729 bp mRNA linear UI-H-EZ1-bbg-h-14-0-UI.s1 NCI CGAP Ch2 Homo sapiens UI-H-EZ1-bbg-h-14-0-UI 3', mRNA sequence.
BQ575741 8Q575741.1 GI:21479058 EST.
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                              Homo sapiens
      Hominidae; Homo
                                                                                 Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                        CGTAGGTGAAAAGGCAG 1321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGACCCGGCTCCACCACACACACACCCCCTAGAGAGAGCGCAGCCATCTGGAGCAAAG
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                                                                                                                                                                                                                                                                                                                 CGTAGGTGAAAAGGCAG
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cDNA clone EST 19-JUN-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: M13 FORWARD POLYA=Yes.
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                      TCAGCGCCACGTGCTACGGCAGCGGCGGGCGGCGACCTACAGCG 1112
                                                                                                                                                                                                                                                                                                                                                                                                                     AGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCACCCATCTCGCTGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCC
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                                                                                                                          GTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCCGGCAGTAACTCGGGCA 1052
                                                                                                                                                                                                                                                                                        ACGGGGAGGAGCCCCCACCCTACCAGGGCCCCCTGCACCCTCCAGCTTCGGGACCCCGAGC
                                                                                                                                                                                                                                                                                                                    ACGGGGAGGAGCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGC
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                                                                                            GTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCAGCAGTAACTCGGGCA
                                                                                                                                                                                           AGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACA
                                                                                                                                                                                                                                    AGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACA
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//clome_lib="NCI_CGAP_Ch2"
//note="Organ: Left Pelvis; Vector: pT773-Pac (Pharmacia)
//note="Organ: Left Pelvis; Vector: pT773-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAG_SEQ=ATCTAATATG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
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'db_xref="taxon:9606"
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Pred. No. 7.5e-244;
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BU602918.1 GI:23254677
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        850 bp mRNA linear ES' AGENCOURT 10016502 NIH_MGC_142 Homo sapiens cDNA clone IMAGE:6497853 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.
1 (bases 1 to 850)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGCAGCGCCGCCCCT 1172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 499.
                                                                                                                                                                                                         /tissue_type="mixed (pool of 40 RNAs)"
/lab host="DHH10B (71-phage-resistant)"
/clone_lib="NIH_MGC_142"
/clone_lib="NIH_MGC_142"
/clone_rector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
/note="vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
/site_2: SfiI (ggccgcctcggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
- 2%, blood - 33.4%, brain - 5.6%, intestine - 2.6%,
/tidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
/ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
5'-ATTCTAGAGGCCGAGGCGGCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH_MGC 141). Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
                                                                                                                                                                used in cloning as follows:
5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="IMAGE: 6497853"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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Query Match

Score 511;

DB 5;

Length 850

Best Local Similarity

99.78;

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RESULT 13
BQ690750
LOCUS
                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                    AGENCOURT_8046394 NIH_MGC_110
5', mal sequence.
BQ690750
BQ690750.1 GI:21816066
                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                         Mammalia; Eutheria;
                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                    Hominidae; Homo.
1 (bases 1 to 890)
                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                            Homo sapiens (human)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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Matches 547; Conserv
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plate: LLCM2368 row: h colu
High quality sequence stop: (
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 1.7e-233;
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DN990606 553 bp mRNA linear EST 17-MAY-2005 TC121025 Human adult whole brain, large insert, pCMV expression library Homo sapiens cDNA clone TC121025 5' similar to Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript

EST 17-MAY-2005

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Matches 54
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Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,LLiu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.
High-throughput cloping of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                 œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Kovacs, KF
High Throughput cDNA Cloning
Origene Technologies, Inc. ( www.origene.com )
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
Email: cDNA@origene.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This EST submission is part of an on-going human full-length cloning project at OriGene Technologies, Inc. Please contact OriGene for access. OriGene Technologies, Inc. OriGene Technologies, Inc. 6 Taft Ct. Suite 100 Rockville, MD 20850 Tel: (301) 340-3188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                CCGCAGGTCTACGCCCCCCCCCCCCCCCACCGACCGCCTTGGCCGTCCCCTTCGCCCAG
                                                                  CCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAG
                                                                                                                                                  TCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAG
                                                                                                                                                                                        TCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAG
                                                                                                                                                                                                                                ATCGTGGTGATGATGGTGATGGTGGTGATCACGTGCCTGACCCAACTACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer: pCMV6 5prime forward vector primer, OriGene
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: Brain; Vector: pCMV6-XL5; Site_1: EcoR1; Site_2: Xho1/Sall compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcripts, cDNA size selection, optimized ligation large inserts into mammalian expression vector, randc clones selected for end sequence verification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Whole brain"
/clone_lib="Human adult whole brain, large insert,
expression library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               full-length genes"
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                                                                                                                                                                                                                                                                                                                                                                                             Score 495; DB 8; 1
Pred. No. 1.7e-232;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 553;
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REFERENCE
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKFZp686K23134 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686K23134 s', mRNA sequence.
                                                                                                                                                                                                                                                           No s1 sequence available.
This clone (DKFZp686K23134) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                                                                                                                                                                                                                                                                                                                                           Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.Wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., et al.)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poustka,A., Albert R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                  Berlin-Charlottenburg, GERMANY;
                                                                                                                                                                                                                                                                                                                           German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wiemann,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX641317.1 GI:34475636
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/clone_lib="686 (symonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2:
cDNA-collection"
                                                              /clone="DKFZp686K23134"
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/lab_host="DH10B"
                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                                                ocation/Qualifiers
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Query Match
Best Local Similarity Matches .524;

35.9%;

Score 474; DB 5; 1 Pred. No. 3.9e-222; Mismatches

Length 572; Indels

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Conservative

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                                                                                                                                    cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2700 row: k column: 15
High quality sequence stop: 468.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BU527705.1 GI:22838146
EST.
                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.
1 (bases 1 to 1068)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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/lab_host="DH10B (phage-resistant)"
                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gccgccggcagcccaargrerectgcacgrgcaactgcaaacgcrctrtrgrrccagage
                                                                                                                                                                                                                          TTTCCGGACGCCACCCGCGGCACTGCCGACGCCCCCGGGGCTGCCGAGGGGAGGCCGGG 140
ATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTG 562
                                                                      GCCGCCGGGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGC
                                                                                                                                            CGCCGCGCCGCCGCCGTCCATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCG
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                                                                                                                      CGCCGCGCCGCCGTCCATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCC
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/note="Organ: lung; Vector: pOTB7; Site_1: ECORI; Site_2:
/note="Organ: lung; Vector: pOTB7; Site_1: ECORI; Site_2:
/note="Organ: lung: Vector: potming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 471; DB 5; Lo
Pred. No. 1.1e-220;
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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BQ691705
LOCUS
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VERSION
KEYWORDS
                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                             JOURNAL
                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                           1 (bases 1 to 655)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
                                                                                                                                                                                                                                                                                                                                                                         AGENCOURT 8046876 NIH MGC 110 5', mRNA sequence. BQ691705
                                                                                                                                                                                                                                                                                                                                       BQ691705.1
EST.
CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                 655 bp
C_110 Homo
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RESULT 18
BU859860
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VERSION
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Plate: LLCM2367 row:
High quality sequence
                                                                                                                964 bp
AGENCOURT 10442713 NIH MGC 107 I
IMAGE:6650839 5', mRNA sequence
BUB59860
Hominidae; Homo.
1 (bases 1 to 964)
                                                                                               BU859860
BU859860.1 GI:24044852
                             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                          Homo sapiens
                                                                      Homo sapiens (human)
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                                                                                                                                                                                                                                                                                           CCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAAGGATAAACAGAAAGGACACCCTCTC 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGGGGCGCATGGAGGGG 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTC
                                                                                                                                                                                                                                                                                                                              CCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAG 1153
                                                                                                                                                                                                                       TAGGGTCCCCAGGGGGCCGGGCTGGGGCTGCGTAGGTGAAAAGGCAG
                                                                                                                                                                                                                                                                            CCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAAAGGATAAACAGAAAGGACACCCTCTC
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quality sequence stop: 645.
Location/Qualifiers
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100.0%; Pred. No. 3.5e-219;
                                                                                                                           mRNA sequence.
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RESULT 19
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TITLE
JOURNAL
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Best Local Similarity
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
  BU539219
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Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: WGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                        CGGGCTGGGGTGCGTAGGTGAAAAGGCAG 1321
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                                                                                                                                                                                                                                                        Conservative
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/lab host="PH108 (phage-resistant)"
/clome_libe"NIH_MGC_107"
/clome_libe"NIH_MGC_107"
/note="Torgan: breast; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRIX/KhoI sites using the following 5' adaptor: GGCACCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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_xref="taxon:9606"
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 782)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 FORWARD
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Unpublished (1997)
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1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAAGGCT.
                                                                                                                                                                                                                                  /clome lib="NCI_CGAP_ED1"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI_CGAP_ED1 is a normalized CDNA library
containing the following tissue(s): Chondrosarcoma cell
line CS5. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:5834635"
/cissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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TAG_LIB=UI-H-ED1
TAG_SEQ=CGTCAAGGCT"
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                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
                                                                                                                             Hominidae; Homo.

1 (Dases 1 to 602)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy
                                                                                                  Tumor Gene Index 
Unpublished (1997)
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing \beta y\colon Dr. M. Bento Soares, University of Iowa
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nilarity 99.6%;
Conservative
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Pred. No. 7.6e-208;
0; Mismatches 2;
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Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD

Location/Qualifiers
1. 602
1. 602
2. /organism="Homo sapiens"
//db xrefs="Homo sapiens"
//db xrefs="Homo sapiens"
//db xrefs="Roxn:9606"
//clone="UI-H-FG1-Bgi-c-12-0-UI"
//clone="UI-H-FG1-Bgi-c-12-0-UI"
//clone="Organ: Enchondroma; Vector: pT773-Pac (Pharmacia)
//note="Organ: Enchondroma containg to Bonaldo, Lennon
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Query Match Best Local Similarity Matches 1180 1120 1060 1240 880 422 482 542 302 362 442; GATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCGGCAGTAACTCGGGCATCAGCGC GGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCT | CGGCCACTACCCGGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCT GGAGGGGACCCGGCTCCACACACACACATCGCGCCCCTAGAGAGGCGCAGCCATCTGGAG 1239 CGGCCACTACCCGGGGTCCTCCCTTCCAGCACCAGCAGCAGTGGGCCGCCCCCCTCCTTGCT CACGTGCTACGGCAGCGGGGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCAT CACGTGCTACGGCAGCGGCGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCAT GATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCGC GGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCT GGAACTGAACCGGGAGTCGGTGCGCGCACACCCCCAAACAGAACCATCTTCGACAGTGACCT GGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCT GGCTGCGTAGGTGAAAAGGCAG 1321 GGAGGGGACCCGGCTCCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAG Conservative 33.5%; 0; Score 442; DB 6; Lo ; Pred. No. 2.3e-206; 161 Mismatches 0 Length Indels 0; Gaps 1179 1119 1059 183 243 363 423 483 999 543

RESULT 22 AY419334

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Best Local Similarity
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens TMEPAI gene, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene trios
Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 These sequences were made by sequencing genomic exons and ordering them based on alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                                                CCACCACACACACACGCCCCCTAGAGAGCCCAGCCATCTGGAGCAAAGAGAAGGATAA 1254
                                                                                                                                                GTCCTCCTTCCAGCACCAGCAGAGCAGTGGGGCCGCCCTCCTTGCTGGAGGGGACCCGGCT 1194
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                                           CCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAA
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|mol_type="genomic DNA"
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VIRTUAL TRANSCRIPT, partial sequence,
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881 GAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTG

Query Match
Best Local Similarity
Matches 441; Conserv

33.4%; Score 441; DB 3; Liarity 100.0%; Pred. No. 7.4e-206; Conservative 0; Mismatches 0;

Length 461; 5; Indels

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UI-E-EJO-ahg-a-10-0-UI.rl UI-E-EJO Homo sapiens cDNA
UI-E-EJO-ahg-a-10-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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BM712680.1 GI:19025938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8889548
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                     / Note = "Torgan: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-ENO is a subtracted CDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGRATCAAGA; lens, CGATTAAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="UI-E-EJO-ahg-a-10-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE optic nerve, retina, RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choroid"
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mol_type="mRNA"

db_xref="taxon:9606"
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'lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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VERSION
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                                                                                                                                                                                                Tissue Procurement: Dr. Gregg Hageman CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                           Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 5224: Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 633)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches
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UI-E-EJO-ahs-f-20-0-UI.rl UI-E-EJO Homo sapiens cDNA clone
UI-E-EJO-ahs-f-20-0-UI 5', mRNA sequence.
                                                                                                                    Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 593-614, ANT rich#Low_complexity (matched compliment) Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                        8889548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              discovery
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                                                                                                                                                                                                                                                                                                          Email: bento-soares@uiowa.edu
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                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                   Location/Qualifiers
'clone="UI-E-EJ0-ahs-f-20-0-UI"
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                                                                                . 633
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ACCESSION VERSION KEYWORDS

ORGANISM

Homo sapiens

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DEFINITION BU624784/c RESULT 25

BU624784 588 bp mRNA 1 UI-H-FG1-bgi-f-22-0-UI.s1 NCI CGAP FG1 Homo UI-H-FG1-bgi-f-22-0-UI 3', mRNA sequence. BU624784 BU624784.1 GI:23290999 EST.

sapiens

EST 23-SEP-2002 CDNA clone

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Matches
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CGTAGGTGAAAAGGCAG
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//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//clone lib="UI-E.EJ0"
//clone lib="UI-E.EJ0"
//note="forgan: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJ0 is a subtracted CDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)1B tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Poveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
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450
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1 (bases 1 to 588)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
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Unpublished (1997)
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                                                                                                                                                                                                                                             GCGGCGGGCGATGGAGGGGCCGCCGCCCACTACAGCGAGGTCATCGGCCACTACCCGG 1133
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                          TCCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATA
                                                                                                                      GGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGGC 1193
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Conservative
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//dev stage="Adult"
//lab host="DH10B (Life Technologies)"
//clone_lib="NCI_CGAP_FG1"
//clone_lib="NCI_CGAP_FG1"
//note="Organ: Enchondroma; Vector: pT7T3-Pac (Pharmacia)
//note="Organ: pt7T3-Pac (Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_SEQ=CGGTCACTC"
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/db_xref="taxon:9606"
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100.0%; Pred. No. 1.9e-199;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Feb 15, 2001 this sequence version replaced Contact: Genoscope
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AL558882 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS0DJ015YF12 5-PRIME, mRNA sequence.
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2 rue Gaston Cremieux, CP 5706 - 91057 EV
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODJ015DC06QP1&c=9945.r.
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1 (bases 1 to 897)
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AGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCCTCGGCCCACC
                                                                                                               AGCCAGGGGCGGAGGAGAGAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCTGGAG
                                                                                                                                                                                                                                    GTGATCACGTGCCTGGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCAC
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                                                                                                                                                                                                                                                                                                                     Conservative
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/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
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/mol_type="mRNA"
/db_xref="taxon:9606"
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cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
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Pred. No. 5.6e-198;
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JOURNAL COMMENT
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                                                                                                                                                                                        Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EWNZ cedex - FRANCE 2 rue Gaston Cremieux, CP 5706 - 91057 EWNZ cedex - FRANCE Email: segref@genoscope.cns.fr Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitogen.
                                                                                                                                                                                                                                                                                                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:30492472. Contact: Genoscope
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AL517150 Homo sapiens NEUROBLASTOMA
CSODA008YB23 3-PRIME, mRNA sequence.
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                                                                                                                                                This sequence belongs to sequence cluster 9945.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODA008CA12NPl&c=9945.r.
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AL517150.3 GI:45653717
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/tissue_type="NEUROBLASTOMA"
/clone_Tib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pcfwSpOrT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                               Location/Qualifiers
                                                           clone="CS0DA008YB23"
                                                                         /db_xref="taxon:9606"
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double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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AGENCOURT 8345390 NIH MGC 110 5', mRNA sequence.
BQ686793
Hominidae; Homo.
1 (bases 1 to 844)
NIH-MGC http://mgc.nci.nih.gov/
                                                                                                 Homo sapiens
                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                      BQ686793.1 GI:21812109
                                                                                                                 Homo sapiens (human)
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Tissue Procurement: ATCC
BU157842
AGENCOURT 7976988 NIH MGC 110 Homo
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http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/lab_host="DH10B (phage-resistant)
/clone_lib="NIH_MGC_110"
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/db_xref="taxon:9606"
/clone="IMAGE:6248044"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2308 row: 1 column: 22
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Tissue Procurement: ATCC
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National Institutes of Health, M
Unpublished (1999)
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BU157842.1 GI:22671752
EST.
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1 (bases 1 to 938)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
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                 AAGGACACCCTCTCTAGGGTCCCCAGGGGGGGCCGGGCTGGGGCTGAGATAGGCC
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/lab host="DH10B (phage-resistant)"
/clome_lib="NII_MGC_110"
/clome_lib="NII_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Organ: cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/clone="IMAGE:6081573"
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/mol_type="mRNA"
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Pred. No. 1.7e-196;
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KEYWORDS
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BU157959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Biom.A.G.E. Corporation
Clone distribution: MGC clone distribution information can
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                                          GGCGCATGGAGGGGCCGCCCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCT
                                                                                                                                      GCGGCCCCTGCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCG
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/db xref="caxon:9606"

/db xref="laxon:9606"

/clone="IMAGE:6084984"

/tissue_type="ductal carcinoma, cell line"

/clone_"IMH_MGC_110"

/clone_"Organ: pancreas; Vector: pOTB7; Site_1: XhoI;

/fite_2: EcoRI; cDNA made by oligo-dT priming.

Site_2: EcoRI; cDNA wising the following 5; adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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Pred. No. 1.7e-196;
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KEYWORDS
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BQ691500
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421
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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5', mRNA sequence.
BQ691500
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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http://image.llnl.gov
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                                                                                                        Similarity
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can
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                                                                                    Conservative
                                                                                                                                                                              /tissue_type="ductal carcinoma, cell line"
/tissue_type="ductal carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_Il0"
/clone_lib="NIH MGC_Il0"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CONA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                 clone="IMAGE:6248217"
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Pred. No. 1.6e-196;
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Hominidae; Homo.
1 (bases 1 to 559)
1 (bases 1 to 559)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B8855409 559 bp mRNA linear BST 29-8EP-7913F05.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAES: 3306369 similar to TR:Q9UJD3 Q9UJD3 DJ718J7.1 ;, mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                    CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                info@image.llnl.gov
Beq primer: -40UP from Gibco
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                                                                                                                                                                                                                                   quality sequence stop: 443.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgapbs-r@mail.nih.gov
Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                 Ph.D
/clone_lib="NCI_CGAP_Brn23"
/note="Organ: brain; 'Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                     /tissue_type="glioblastoma/lab_host="DH10B"
                                                                                                                            clone="IMAGE: 3306369"
                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
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Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                     Coordinated Laboratory for Computational (University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BU730650
UI-E-CI1-afq-o-09-0-UI.sl UI-E-CI1 Homo sapiens cDNA
UI-E-CI1-afq-o-09-0-UI 3', mRNA sequence.
                                                                                                                     Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                             1 (bases 1 to 629)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
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EST.
                                                                                                                                                                                                                 Contact: Soares, MB
                                                                                                                                                                                                                                   8889548
                                                                                                                                                                                                                                                       Genome Res. 6 (9),
                                                                                                                                                                                                                                                                           discovery
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                             Normalization and subtraction: two
                                                                                                 Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                     Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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Pred. No. 5.1e-194;
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                   1400 bp AGENCOURT 6598258 NIH MGC 41 Homo 5', mRNA sequence.
BM559329
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BM559329.1 GI:18802821
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UI-E-CII is a normalized CDNA library containing the
following tissue(s): RPE and Choroid. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand CDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded CDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pTTJ-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is ACCTA.
This library was created for the program, Gene Discovery
in the Visual System, supported by National Eye Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_TISSUE=RPE and Choroid
TAG_LIB=UI-E-CI1
TAG_SEQ=ACCTA"
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/tissue_type="RPE and Choroid"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant
/clone_lib="UI-E-CII"
/note="Organ: eye; Vector: pT7T3-Pac (pharmacia) with a
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; Pred. No. 5e-194;
                                                                                  sapiens cDNA clone
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Location/Qualifiers
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg,
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1 (bases 1 to 1400)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: WGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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/lab host="DH10B (phage-resistant)"
/clome libe"NIH MGC 41"
/clome libe"NIH MGC 
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/db_xref="taxon:9606"
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Pred. No. 1.3e-188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 730)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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    Conservative
                                                                                                                                                                            constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATRCC. This library was created for the program, Gene CGCGTATRCC in the Visual System, supported by National Eye
                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EO1 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was
                                                                                                                                                                 Institute (NEI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="fetal"
/lab_host="DH10B (Life Technologies)
/clone_lib="UI-E-EO1"
                                                                                                   TAG_SEQ=CGCGTATACC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="fetal eye"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="UI-E-E01-aid-p-09-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'mol_type="mRNA"
'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                         TISSUE=human fetal eye
LIB=UI-E-EO1
                   30.4%;
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                   Score 401; DB 3;
Pred. No. 3.9e-186;
    Mismatches
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REFERENCE
AUTHORS
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ORGANISM
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Email: paul-mccray@uiowa.edu

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM974296 626 bp mRNA linear UI-CF-EC1-aca-k-23-0-UI.sl UI-CF-EC1 Homo sapiens UI-CF-EC1-aca-k-23-0-UI 3', mRNA sequence.
                                                                                                                                                Tel: 319 356 4866
Fax: 319 356 7171
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                             University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                       8889548
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                                                                                                                                                                                                                                                                                                                                    discovery
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Bonaldo, M.F., Lennor
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CN296134.1 GI:43312548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Clone="UI-CP-EC1-acca-k-23-0-UI"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab host="PH108 (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EC1"
/clone_lib="UI-CF-EC1"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
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TAG LIB=UI-CF-EC1
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db_xref="taxon:9606"
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; Pred. No. 3.8e-185;
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sapiens cDNA 5', mRNA
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POCAR

DEFINITION BU683523/c RESULT 38

BU683523 728 bp mRNA linear EST 07-0 UI-CF-EC1-acg-e-09-0-UI.sl UI-CF-EC1 Homo sapiens cDNA clone

EST 07-OCT-2002

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COMMENT
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Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Brandenberger R
Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, Lebkowski, J and Stanton, L.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae; Homo.
1 (bases 1 to 544)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Insert Length: 544 Std Error:
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                                                                                                                                                                                                                                                                                                                                                                                   TCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCCTGCCCCCCCAGCAGTAACT
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 GGGGCCGGGCTGGGGCTGCGTAGGTGAAAAGGCAG 1321
                                                                                   CAGCCATCTGGAGCAAAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGG 1286
                                                                                                                                                         CGCCCTCCCTTGCAGGGGGACCCGGCTCCACCACACACATCGCGCCCCTAGAGAGCG 1226
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                                               CAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGG
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/db_xref="taxon:9606"
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Pred. No. 3.6e-183;
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543
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Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: M13 FORWARD
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                                   CTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGAC
                                                                                                     GAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAG
    ĊTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGAC
                                                                              GAGGAGCCCCCACCCTACCAGGCCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAG
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laldo, M.P., Lennon, G. and Soares, M.B.
laldo, M.P., Lennon, G. and Soares, M.B.
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                                                                                                                                                            Conservative
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//dev stage="Adult and Fetal"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//clome lib="UI-CF-EC1"
//clome lib="UI-CF-EC1" vector: pT7T3-Pac (Pharmacia) with a
//note="Drogan: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EC1 is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(ACT) 18 tail. The sequence tag for this library is
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tissue_type="Lung"
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'db_xref="taxon:9606"
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                                                                                                                                                                             29.8%;
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                                                                                                                                                                               Score 393; DB 5;
Pred. No. 3.4e-182;
                                                                                                                                                            Mismatches
                                                                                                                                                                                                  Length 728;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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1 (bases 1 to 973)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, M
Unpublished (1999)
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5', mRNA sequence.
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Location/Qualifiers
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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/note="Torgan: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                  /tissue_type="ductal carcinoma, cel
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/clone_lib="NIH_MGC_110"
                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                          clone="IMAGE:6082799"
                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
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570 bp mRNA linear EST:
UI-H-EZ1-bbf-f-09-0-UI.s1 NCI_CGAP_Ch2 Homo sapiens cDNA
UI-H-EZ1-bbf-f-09-0-UI 3', mRNA sequence.
                                                           Seq primer: M13 FORWARD POLYA=Yes.
                                                                                                                                                                                                Orthoapedics
                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian,
                                                                                                                                                                                                                                                        Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo.
1 (bases 1 to 570)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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EST.
                                                                                                                                                                                                                                                                                                 Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained
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/organiqm="Homo sapiens"
                                      Location/Qualifiers
                                                                                              Bento Soares, bento-soares@uiowa.edu
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Pred. No. le-180;
0; Mismatches
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5', mRNA sequence.
CB044440
    Hominidae; Homo.
1 (bases 1 to 563)
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                GGGCTGCGTAGGTGAAAAGGCAG 1321
                                                                                                                                                                                                                                                                                                                       GGGCTGCGTAGGTGAAAAGGCAG 161
                                                                                                                                                                                                                                                                                                                                                                                                     GCAAAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGGCCGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                              GCAAAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCCGGGCTG 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGGCCACTACCCGGGGTCCTCCCTTCCAGCACCAGCAGCAGTGGGCCGCCCCTCCTTGC 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCACGTGCTACGGCAGCGGCGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCACGTGCTACGGCAGCGGCGGGCGCATGGAGGGGCCGCCGCCGCCCACCTACAGCGAGGTCA 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGATGGATAGTGCCAGGCTGGCCGGCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGTGGGCCGCCCCTCCTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone libe"NCI CGAP Ch2"
/clone libe"NCI CGAP Ch2"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EccR I; Site 2: Not I;
with a modified polylinker; Site 1: EccR I; Site 2: Not I;
NCI CGAP Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-EZ1-bbf-f-09-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Adult"
/lab_host="DH10B (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="Chondrosarcoma Grade
                                                                                                                                             GI:27788087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
3e-177;
                                                                                                                                                                                                       mRNA linear EST 17-JAN-2003 sapiens cDNA clone IMAGE:3271656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 570;
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304

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      DEFINITION
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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BM713900 552 bp mRNA linear EST 28 UI-E-EJO-ahq-e-07-0-UI.rl UI-E-EJO Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: LLAM8009 row: E column: 1
Seq primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       info@image.linl.gov
Plate: LLAM8009 ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: NCI-CGAP clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Arrayed by: The I.M.A.G.B. Consortium/LLNL
                                                                                                                                                CGTAGGTGAAAAGGCAG 1321
                                                                                                                                                                                                                                                                                                                         ACTACCCGGGGTCCTTCCCAGCACCAGCAGCAGTGGGCCGCCCCCCTCCTTGCTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGG
                                                                                                                                                                                                            AGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGGCCGGGCTGGGGCTG
                                                                                                                                                                                                                                                   AGAAGGATAAACAGAAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCGGGCTGGGGGCTG 1304
                                                                                                                                                                                                                                                                                              ACTACCCGGGGTCCTTCCAGCACCAGCAGCAGTGGGCCGCCCCCTCCTTGCTGGAGG
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                                                                                                                            CGTAGGTGAAAAGGCAG
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/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="IMAGE:3271656"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.5%; Score 377; DB 6; Length 563; 100.0%; Pred. No. 2.7e-174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             host="DH10B"
                                                                                                                            386
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                       EST 28-FEB-2002
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1004 GATAGTGCCAGGCTGGGCGGCCCTGCCCCCAGCAGTAACTCGGGCATCAGCGCCACG

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944 CTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATG

Mismatches

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REFERENCE
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ORGANISM
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KEYWORDS
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                         Query Match
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   Local Similarity
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BM713900
BM713900.1 GI:19027158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA sequence: $21-543, >POLY_A#Simple_repeat

Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: Dr. Gregg Hageman

CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Iowa
375 Newton Road, 4156 MEBRF,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coordinated Laboratory for Computational Genomics
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 552)
                                                                                                          /dev stage="fetal and adult"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//clone_lib="U1-E-EJ0"
//clone_ribe="U1-E-EJ0"
//clone_ribe="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
//note="Porgan: eye; Vector: pT7T3-Pac (Pharmacia) with a
//note="Porgan: eye; Vector: pT7T3-Pac (Pharmacia) with a
//note="Porgan: eye; Vector: EcoR I; Site_2: Not I;
U1-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGANTCAGGA; lens, CGATTAGCGA; eye anterior segment,
AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="UI-E-EJ0-ahq-e-07-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic_nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choroid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:9606"
27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _type="mRNA"
Score 365; DB 3; Logical Pred. No. 2.3e-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         two
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   approaches
                                   Length 552
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KEYWORDS
SOURCE
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TITLE
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                       Query Match 27.1%;
Best Local Similarity 99.8%;
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  Matches 408;
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2318 row: h column: 10
High quality sequence start: 159
High quality sequence stop: 554.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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AGENCOURT 8045602 NIH_MGC_110
5', MRNA Sequence.
BU174654
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National Institutes of Health, M
Unpublished (1999)
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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  Conservativo
                                                                                                          /clone="IMAGE:6085305"
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Site_2: EcoRI; cDNA made by oligo-dT priming:
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
Score 358; DB 5;
Pred. No. 6.2e-165;
0; Mismatches 1;
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AGENCOURT 10442327 NIH MGC 107 Homo
IMAGE:6650815 5', mRNA sequence.
BUB59841
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2896 row: k column: 07
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Tissue Procurement: ATCC
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1 (bases 1 to 646)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                            High quality sequence stop: 551.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
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Query Match

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Similarity

Score 348; DB 5; ? Pred. No. 5.5e-160; D; Mismatches 2;

Length 646; Indels

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(Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

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RESULT 45
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2 rue Gaston Cremieux, CP 5706 - 9105 FWAY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 9105 FWAY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                           On May 5, 2003 this sequence version replaced gi:30378625. Contact: Genoscope
                                                                                                                                                                                                                                                                               Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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BX362396
BX362396.2 GI:46307643
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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               http://www.genoscope.cns.fr/cdna?s=CSODJ014CG08NP1&c=9945.
Location/Qualifiers
                                                         For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.
1 (bases 1 to 867)
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                                                                                                                                                                                                                                                                                                                                            899 bp
AGENCOURT 7975303 NIH MGC_110 Homo
5', mRNA sequence.
BU196912
                                                                                                     Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                EST
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Comporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
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/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="CSDJ014YN15"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
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Pred. No. 4.6e-155;
D; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 522 CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGGTGATGGTGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM676516 547 bp mRNA linear EST 27
UI-E-EJO-ahq-e-07-0-UI.s2 UI-E-EJO Homo sapiens cDNA clone
UI-E-EJO-ahq-e-07-0-UI 3', mRNA sequence.
Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road 4156 MEBRF, Iowa City, IA 5224:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: LLCM2311
                                                                                                                                                                                                                                Hominidae; Homo.
1 (bases 1 to 547)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                      Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM676516.1 GI:18986412
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                                                                                                                                        8889548
                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
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Location/Qualifiers
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/tissue_type="ductal carcinoma, cell line"
/lab host="DH108 (phage-resistant)"
/clone_lib="NIH MCC_110"
/clone_lib="NIH MCC_110"
/note="Torgan: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Torgan: pancreas; Vector: pancr
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_xref="taxon:9606"
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Pred. No.
      MEBRF, Iowa City, IA 52242, USA
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nes 377; Conserv
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Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
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Fax: 319 335 9565
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GAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCCGGGCTGGGGCT 1303
                                                                                           GGGACCCGGCTCCACCACACACACATGGGGCCCCTAGAGAGGCGCAGCCATCTGGAGCAAA 1243
                                                                                                                                                                                   CTGAACCGGGAGTCGGTGCGCGCACCCCAAACAGAACCATCTTCGACAGTGACCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATG
                                                              GGGACCCGGCTCCACCACACACACACCTCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAA
                                                                                                                                                         TGNTACGGCAGCGGGGGGGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCGGC
                                                                                                                                                                                                                                                                                                                                             GATAGTGCCAGGCTGGGCGCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Torgan: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-B-EJO is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT).18 tail. The sequence tags for this library are: fetal eyes, AGRATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_TISSUE=human eye anterior segment
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/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ0"
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Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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EST.
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613 bp mRNA linear EST 01-MAY-2001
60262921/F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4753829 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM10614 row: b column: 06
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Homo sapiens
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                                                                                                                                   ATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTG 1177
                                                                                                                                                                                                                                                             GCCACGTGCTACGGCAGCGGCGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTC
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                                                                                                                                                                                                                                                                                                                                       CTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCAGCAGTAACTCGGGCATCAGC
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/lab_host="MAIO8 (T1 phage-resistant)"
/clone lib="NCI CGAP Skn4"
/note="Corgan: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Corgan: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/mol_type="mRNA"
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/clone="IMAGE:4753829"
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Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 324; DB 2; L
Pred. No. 3.8e-148;
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MMSP0052_A05 MMSP Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ted@locke.he.washington.edu
Similar to GenBank entry BC015918 BC015918 Homo sapiens,
MGC:20374 IMAGE:4559576, mRNA, complete cds. 10/2001
Plate: MMSP0052 row: A column: 05.
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Katze,M.G., Bumgarner,R., Korth,M., Feldman,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta
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Fax: 206 732 6055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Holzman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holzman, T.
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                         TCCTTGCTGGAGGGGACCCGGCTCCACCACACACACATCGCGCCCCTAGAGAG
                                                                                        GAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGCAGTGGGCCGCCC
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/dev_stage="adult"
/clone_lib="MMSP"
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/db_xref="taxon:9544"
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Unpublished (1997)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                            GCTACGGCAGCGGCGCATGGAGGGGCCGCCCACCTACAGCGAGGTCATCGGCC
                                                                       GCTACGGCAGCGGCGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCC 1124
                                                                                                                                ATAGTGCCAGGCTGGGCGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGT 1064
                                                                                                                                                              TGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
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100.0%; Pred. No. 2.7e-137;
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Search completed: February 28, 2006, 11:47:21 Job time : 5868 secs

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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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7: /cgn2_6/ptodata/1/ina/PE_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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US-09-949-016-17765
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APPLICANT: XU, LINDA L.
APPLICANT: XU, LINDA L.
APPLICANT: XU, TAKEHKO
APPLICANT: TAKEHKO
APPLICANT: PEGAWA, TAKEHKO
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
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TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: PROSTATE-US/09/769,482
CURRENT APPLICATION NUMBER: US/09/769,482
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,772
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
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APPLICANT: XU, LINDA
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                                                                                                                                                    RESULT 2
US-09-769-482-2
                                                                                                          Sequence 2, Application US/09769482 Patent No. 6566130 GENERAL INFORMATION:
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              APPLICANT: SRIVASTAVA, SHIV
APPLICANT: MOUL, JUDD W.
APPLICANT: XU, LINDA L.
APPLICANT: SEGAWA, TAKEHIKO
APPLICANT: SEGAWA, TAKEHIKO
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: POWINCLEOTIDE ARRAY
FILE REFERENCE: 04995.0057-00000
CURRENT APPLICATION NUMBER: US/09/769,482
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FRIOR APPLICATION NUMBER: 60/178,772
FRIOR FILING DATE: 2000-01-28
FRIOR APPLICATION NUMBER: 60/179,045
FRIOR APPLICATION NUMBER: 60/179,045
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 759
TYPE: DNA
ORGANISM: Homo sapiens
US-09-769-482-2
 RESULT 3
US-09-640-211A-146/c
; Sequence 146, Appl:
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  Application US/09640211A
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0; Mismatches
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124 701 184 161 761 761 244 821 821 304 941

INFORMATION:

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US-09-640-211A-1340/c
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CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1198
LENGTH: 359
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SEQ ID NO 146
LENGTH: 640
TYPE: DNA
ORGANISM: Eucalyptus grandis
S-09-640-211A-146
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                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                             Sequence 1340, Application US/09640211A Patent No. 6833446
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APPLICANT:
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                                     APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Shenk, Michael A. APPLICANT: McGrath, Annette APPLICANT: Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Modification of Gene Transcription
                                                                                                                                           APPLICANT: Wood, Marion APPLICANT: Shenk, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Eucalyptus grandis
                   URRENT APPLICATION NUMBER: US/09/640,211A
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Glenn, Matthew
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2000-08-16
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US-10-104-047-700/c
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; ORGANISM: Human
US-09-949-016-13247
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SEQ ID NO 700
LENGTH.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1340
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Patent No. 6943241
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
                                                                       SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13247
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                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full length cDNA
FILE REFERENCE: H1-A0105
                                                                                                                         PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768.
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2002-03-25
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                                                                                                               NUMBER OF SEQ ID NOS:
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ORGANISM: Homo sapiens
                                       TYPE: DNA
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100.0%; Pred. No. 0.00097;
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Pred. No.
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Query Match Best Local Similarity

2.3%;

Score 30; DB 3; Pred. No. 0.0023;

Length 11729;

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US-09-949-016-15127
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                                                                             US-09-949-016-1263
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Patent No. 6812339
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                                     Query Match
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NAME/KEY: misc_feature
LOCATION: (1)...(142783)
OTHER INFORMATION: n = A,T,C or G
-09-949-016-15127
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                       NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: CL001307
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TYPE: DNA
ORGANISM: Human
                                                                                             ORGANISM: Human
                                                                                                                   TYPE: DNA
                                                                                                                                     ENGTH: 3430
Local Similarity 100.0%; Pred. No. 0.0 nes 29; Conservative 0; Mismatches
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%; Pred. No. 0.0
0; Mismatches
                   Score 29;
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                   DB 3;
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Query Match
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US-09-949-016-17419/c
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISSASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION UNMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASESEQ for Windows Version 4.0
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LENGTH: 9406
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                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 17419
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Matches
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: CL001307
                                                                                                  NAME/KEY: misc_feature
LOCATION: (1)...(13832)
OTHER INFORMATION: n =
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                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                       ORGANISM: Human
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Local Similarity es 29; Conserv
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Conservative
                 2.2%; Score 29; DB 3; Length 13832; 100.0%; Pred. No. 0.0061;
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Pred. No. 0.0063;
Mismatches
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US-09-949-016-12052/c
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Best Local !
                                                                                Query Match
Best Local
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                                                                Matches
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-09-949-016-13765
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-09-949-016-12052
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 12052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20
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IITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 20701
                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/237,768 FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/241,755
FILING DATE: 2000-10-20
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US-09-086-010-1
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US-09-236-097-7
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                                                                                                                                                                                      Sequence 1, Application US/09086010
Patent No. 6274338
GENERAL INFORMATION:
APPLICANT: Glimcher, Laurie H.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                    Matches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
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MEDIUM TYPE: 1.44 mes
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                              NUMBER OF SEQUENCES:
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CLASSIFICATION: 435
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                                            COUNTRY:
                                                                               CITY: Boston
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                                                                                            28 State Street
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Twinhead* Slimnote
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                                                                                                                                                         , Laurie H. et al.
Human c-Maf Compositions
Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MS DOS version 6.2,
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Davis Highway, Suite 207
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COMPUTER:

IBM PC compatible

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RESULT 17
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; LOCATION: (1)..(1203)
US-09-879-312A-1
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                                                                                                                                                                                                                                                                                                                                         APPLICANT: GLIMCHER, LAURIE H.
APPLICANT: DOUHAN III, JOHN
TITLE OF INVENTION: HUMAN C-MAF COMPOSITIONS AN
FILE REFERENCE: HUI-027CPDV1
CURRENT APPLICATION NUMBER: US/09/879,312A
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 09/086,010
PRIOR PILING DATE: 1998-05-27
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 3.3 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local Similarity 100.0%; P
Matches 28; Conservative 0;
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PILING DATE: 2-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: KATA, Catherine J.
REGISTRATION NUMBER: 41,106
REPERENCE/DOCKET NUMBER: HUI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                           LENGTH: 1203
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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RESULT 18
US-07-751-8918-1
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GENERAL INFORMATION:
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Best Local Similarity
Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-53
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 3765 base pairs
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TELEFAX: 762829
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                                                                                   Fu, Ying-hui
TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                      APPLICANT: Caskey, C. T.
Nelson, David L.
                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas D. Paul
                                                                                                                                                                                                                                                                                                                               44
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CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                GGCGGCGGCGGCGGCGGAGGCG 71
                                           STREET: 1301 McKinney, Suite 5100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1301 McKinney, Suite 5100
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Nelson, David L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pieretti, Maura
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                     Warren, Stephen T.
Oostra, Ben A.
                                                                                                                                                                       Pieretti, Maura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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ZIP: 77010-3095

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                            APPLICATION NUMBER: US/08/455,073A FILING DATE: 31-MAY-1995 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Fragile X Related Proteins, Compositions And Methods TITLE OF INVENTION: Of Making And Using The Same NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5876949ris STREET: One Liberty Place, 46th floor
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mikiko C. APPLICANT: Yan Zhang
                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gideon Dreyfuss
                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/751,891B
FILING DATE: 29-Aug-1991
CLASSIFICATION: <Unknown>
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 713/651-5246
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                                                                                                                 , MOLECULE TYPE:
US-08-457-273B-41
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                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                 TELEFAX: 919-854-1401 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,27:
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 10348 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Mouse Model for Huntington's Disease and
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                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                       TYPE: ... STRANDEDNESS: SI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 27627
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es 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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: No. 5849995th Carolina
 GAGGAGGCGGCGGCGGCGGCGGCGG 442
                        GAGGAGGCGGCGGCGGCGGCGGCGG 78
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                                                         Conservative
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                                                                     2.1%; Score 28; DB 2;
100.0%; Pred. No. 0.017;
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Pred. No.
                                                                                                                                                                                                                                                                            3477-85A
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                                                          Mismatches
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                                                                                    Length 10348;
                                                            Indels
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RESULT 22
US-09-041-886-14/c
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APPLICANT: Lanahan, Anthony
APPLICANT: Lanahan, Anthony
APPLICANT: Worley, Paul
APPLICANT: Snyder, Solomon
TITLE OF INVENTION: Huntingtin-associated protein
FILE REFERENCE: 01107.52271
CURRENT APPLICATION NUMBER: US/08/556,419C
CURRENT FILING DATE: 1995-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ross, Christop
APPLICANT: Li, Xiao-Jiang
APPLICANT: Li, Shi-Hua
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                                                                                                         TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 14:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 10348
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharro
 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                    STRANDEDNESS:
TOPOLOGY: lin
                                                 LENGTH: 10348 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Diego
STATE: California
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                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                        United States
                    linear
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DNA (genomic)
                                 single
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100.0%; Pred. No. 0.017;
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; NAME/KEY:
; LOCATION:
US-09-041-886-14
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RESULT 24
US-08-453-265-5/c
                                                                                                                                                                                                 US-08-246-982A-5
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                                                                                                                                  Matches
                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: May 20, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLDStein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3880002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                FEATURE:
NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Duyao, mader r.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                              LENGTH: 10366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                  469 GAGGAGGCGGCGGCGGCGGCGGCGG 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GAGGAGGCGGCGGCGGCGGCGGCGG 78
                                                                                               51 GAGGAGGCGGCGGCGGCGGCGGCGG 78
                                                                                                                                28;
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1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ambrose,
                                                                                                                                  Conservative
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316..9748
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316..9748
                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                 Score 28; DB 2; Pred. No. 0.017;
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Pred. No.
                                                                                                                                   Mismatches
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Sequence 5, Application US/08453265 Patent No. 5693757

PPLICANT:

Ambrose,

Christine M.

MacDonald, Marcy E.

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US-09-949-016-17589
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Best Local Similarity
                                                                      SOFTWARE: Fast
SEQ ID NO 17589
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17589, Application US/09949016
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, VC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                     CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                                                                                                                                                                               FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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NAME/KEY:
LOCATION:
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ORGANISM: Human
9-949-016-17589
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TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            469 GAGGAGGCGGCGGCGGCGGCGGCGGCGG 442
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                                                                                           FastSEQ for Windows Version
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                                                                                                                                2000-09-08
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100.0%; Pred. No. 0.017;
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US-09-949-016-15437/c
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; ORGANISM: Homo sapiens
US-09-854-133-418
              Query Match
Best Local Similarity
"hebs 27; Conserv?
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                                                                                                     ; ORGANISM: Human
US-09-949-016-15437
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Best Local Similarity
Matches 28; Conserv
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Patent No. 6812339
GENERAL INFORMATION:
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                                                                                                                                                                            SEQ ID NO 15437
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APPLICANT:
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APPLICANT: Mohamath, Raodol
APPLICANT: Henderson, Robe
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CURRENT APPLICATION NUMBER: US/09/854,133
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: CL001307
                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 402
                                                                                                                                                           ENGTH:
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mes 27; Conserv
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56 GGCGGCGGCGGCGGCGGAGGC 82
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                                                                                                                                                           8983
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Henderson, Robert A.
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                               2.0%; Score 27; DB larity 100.0%; Pred. No. 0. Conservative 0; Mismatches
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Pred. No. 0.06;
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Pred. No. 0.015;
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                                                    DB 3;
                                                                     Length 8983;
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US-09-827-688-8
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                                                                               US-09-325-932A-2/c
                                                                                                 RESULT 30
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US-09-827-688-8/c
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
               Sequence 2, Application US/09325932A Patent No. 6451604 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 8
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APPLICANT: KINSEY, BERMA
APPLICANT: BHOGAL, BALBIR
APPLICANT: BHOGAL, BALBIR
TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: AGENTS
TITLE REFERENCE: P01949US1/10004014
CURRENT APPLICATION NUMBER: US/09/827,688
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/195,680
PRIOR APPLICATION NUMBER: 60/195,680
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KINSEY, BERMA
APPLICANT: BHOGAL, BALBIR
TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES
TITLE OF INVENTION: AGENTS
FILE REFERENCE: P01949US1/10004014
CURRENT APPLICATION NUMBER: US/09/827,688
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/195,680
PRIOR APPLICATION NUMBER: 60/195,680
PRIOR FILING DATE: 2000-04-07
   APPLICANT:
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SOFTWARE: PatentIn version 3.0
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ORGANISM: HERPESVIRUS 2
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ORGANISM: HERPESVIRUS
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Flinn, Barry
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100.0%; Pred. No. 0.036;
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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
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; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-325-932A-2
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US-09-436-699C-5/c
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 46860
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SEQ ID NO 2
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Best Local Similarity
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Best Local Similarity
                                                   APPLICANT: Famodu, Omolayo O.
APPLICANT: Simmons, Carl
TITLE OF INVENTION: Plant Aminoacyl-trnA Synthetases
FILE REFERENCE: BB1266 US NA
CURRENT APPLICATION NUMBER: US/09/436,699C
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: 60/107,276
PRIOR APPLICATION NUMBER: 60/107,276
PRIOR FILING DATE: 1998-11-05
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
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NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0.16;
0; Mismatches
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Pred. No.
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NAME/KEY: unsure
LOCATION: (354)
OTHER INFORMATION:
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              COCATION: (618)
OTHER INFORMATION: n
                        NAME/KEY: unsure
LOCATION: (618)
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OTHER INFORMATION:
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NAME/KEY: unsure
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THER INFORMATION:
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THER INFORMATION:
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THER INFORMATION:
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THER INFORMATION:
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OCATION: (511)
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RESULT 33
US-09-436-699C-19/c
; Sequence 19, Application US/09436699C
; Patent No. 6696619
; Patent No. 6696619
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Best Local Similarity
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US-09-922-364A-15
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Best Local Similarity
Matches 26; Conserv
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SEQ ID NO 19
LENGTH: 1719
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APPLICANT: Famodu, Omolayo O.
APPLICANT: Simmons, Carl
TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetases
FILE REFERENCE: BB1266 US NA
CURRENT APPLICATION NUMBER: US/09/436,699C
CURRENT FILING DATE: 2002-09-30
                                                                                                                                                                                                                                                                                                                Sequence 15, Application Patent No. 6692937
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Triticum aestivum O9-436-699C-19
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PRIOR FILING DATE: 1998-11-05
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OTHER INFORMATION: n =
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LOCATION: (641)
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                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                       Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels
Thereof
                                                                                                                                                                                                                                                                      APPLICANT: Adelman, John P.
Maylie, James
Bond, Chris T.
                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                               NUMBER OF SEQUENCES:
 CURRENT
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                                                                                                                     STATE: California
                                                                                                                                STREET: Two Embarcadero
               SOFTWARE: PatentIn Release
                                                                                       ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                              Application US/09922364A
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llarity 100.0%;
Conservative (
APPLICATION DATA:
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Pred. No.
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Pred. No.
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                                                                                                                                                 Townsend and Crew LLP Center, Eighth Floor
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               #1.0,
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                 Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application Patent No. 6797486
GENERAL INFORMATION:
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LENGTH: 1740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                         ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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OTHER INFORMATION: /note= "rat sma.calcium-activated potassium channel protein 2 (rSK2) CDMA"
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Small and Intermediate Conductance,
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Adelman, John P.
Maylie, James
Bond, Chris T.
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                                                                                                                                                                                                              STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
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FILING DATE: 03-Aug-2001
                                                                                                                                                                                                                                    CITY: San Francisco
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FILING DATE: 10-Mar-1999
                        APPLICATION NUMBER: US/09/254,590
                                                                                                                                                                                               COUNTRY: USA
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RESULT 36
US-10-115-415-15
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Patent No. 6828122
GENERAL INFORMATION:
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           ZIP: 94111.3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,415
FILING DATE: 02-Apr-2002
CLASSIFICATION: JATA:
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         calcium-activated potassium channel protein 2 (rSK2) cDNA" SEQUENCE DESCRIPTION: SEQ ID.NO: 15:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Weber, Kenneth #
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bond, Chris T.
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/11
FILING DATE: 10-SEP-1997
                                                                                                                                                                                                                                                                             STATE: California
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                                                                                                                                                                                                                                                       COUNTRY: USA
APPLICATION NUMBER: US/09/254,590
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Pred. No. 0.14;
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Patent No. 6828123
GENERAL INFORMATION:
APPLICANT: Adel
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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SEQUENCE DESCRIPTION: SEQ ID NO: 15:
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                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Small and Intermediate Conductance
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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STRANDEDNESS: single
TOPOLOGY: linear
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APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APPL-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
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                                                            APPLICATION NUMBER: US/10/116,260 FILING DATE: 03-Apr-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                             STATE: California
                                                                                                                                                                                                                                                                                                              CITY: San Francisco
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
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                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30
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Maylie, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1740;
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US-10-115-671-15
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Best Local Similarity
Matches 26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application Patent No. 6828420 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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TELEFAX: (415) 576-0
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: WO PCT/US97/16033 FILING DATE: 10-SEP-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
53 GGAGGCGGCGGCGGCGGCGGCGG 78
                                                                                                                                                                                        LOCATION: 1..1740
OTHER INFORMATION: /note= "rat sma
calcium-activated potassium channel
protein 2 (rSK2) cDNA"
                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/026,451 FILING DATE: 11-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/045,233 FILING DATE: 17-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/040,052
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 1740 base pairs
                                              2.0%; Score 26; DB 3; llarity 100.0%; Pred. No. 0.14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   576-0300
                                                                                                                                                                                                                                           /note= "rat small conductance
                                                       <u>.</u>
                                                                                                 Length 1740;
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262 GGAGGCGGCGGCGGCGGCGGCGG 0; Gaps

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Flom PC compatible
COMPUTER: PC DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
SOFTWARE: PATENTIN RELEASE #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,671
FILING DATE: 03-Apr-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA: NUMBER OF SAFETHING ADDRESS:

CORRESPONDENCE ADDRESS:

Townsend and Townsend and Crew LLF

ADDRESSEE: Townsend and Townsend and Crew LLF

ADDRESSEE: Townsend and Townsend and Crew LLF NUMBER OF SEQUENCES: 48 Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof APPLICANT: Adelman, John P. Maylie, James STATE: California APPLICATION NUMBER: US/09/254,590 FILING DATE: 10-Mar-1999 APPLICATION NUMBER: US 60/026,451 ZIP: 94111-3834 CITY: San Francisco Application US/10115671 Maylie, James Bond, Chris T. Version #1.30

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Applicati
Patent No. 6894147
GENERAL INFORMATION:
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Best Local
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SEQUENCE CHARACTERISTICS:
LENGTH: 1740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..1740
OTHER INFORMATION: /note= "rat smalcalcium-activated potassium channel protein 2 (rSK2) CDMA"
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: line
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REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
                                                                              APPLICATION NUMBER: US/10/115,695
PILING DATE: 03-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Silvia, Christopher P. TITLE OF INVENTION: Small and Intermediate Conductance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Adelman, John P.
Maylie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
                                     APPLICATION NUMBER: US/09/254,590 FILING DATE: 10-Mar-1999
                                                                                                                                                                                                                                                                                                                                       STATE: California
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TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
FILING DATE: 11-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP
                   APPLICATION NUMBER: US 60/026,451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.0%; Score 26; DB 3;
100.0%; Pred. No. 0.14;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium-Activated Potassium Channels and Uses
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RESULT 40
US-09-780-173A-10
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NESULT 41
US-08-819-177-2/c
US-08-819177-2/c
; Sequence 2, Application US/08819177
; Patent No. 6043083
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                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (344)...(1396)
US-09-780-173A-10
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                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: RTS-0165
CURRENT APPLICATION NUMBER: US/09/780,173A
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 95
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09780173A Patent No. 6455307 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                        Matches
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA PRIME EXPRESSION
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IOCATION: 1.1740
OTHER INFORMATION: /note= "rat smaler calcium-activated potassium channel protein 2 (rSK2) cDNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                 278
                                                                                                                                                   380 CCCCGCGCCCCGCGCGCGCCGC 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                    l Similarity
26; Conserv
                                                                                                                 CCCCGCGCCCCGCGCCGCCGCCGC 303
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
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                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                         Score 26; DB 3; Pred. No. 0.14;
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Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "rat small conductance,
                                                                                                                                                                                        Mismatches
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ENERAL INFORMATION:

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US-09-949-016-3381
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APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                              Sequence 3381, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 180...2159
OTHER INFORMATION: JIP-1 cDNA
:-08-819-177-2
                                                                                                CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                          FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/
FILING DATE: 28 April 1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fasse, J. Peter
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Coding Sequence LOCATION: 180...2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                          138 GGAGGCGGCGGCGGCGGCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                             53 GGAGGCGGCGGCGGCGGCGGCGG 78
                                   LING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2832 base pairs
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YSTEM: Windows95
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for Windows Version 4.0
                               2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INHIBITORS OF THE JNK SIGNAL TRANSDUCTION PATHWAY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.0%; Score 26; 00.0%; Pred. No.
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0.14;
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RESULT 44 US-09-402-214-1/c

Patent No. Sequence

1, 10, 662091 INFORMATION

Application US/09402214

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; LENGTH: 2891
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
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US-08-859-201-1/c
                                                                                                 LOCATION:
US-08-859-201-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08859201 Patent No. 5880261
                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Waeber, G
APPLICANT: Nicod, P
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                            FILING DATE: 03-APR-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: / CALLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLE OF INVENTION:
                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 15-MAY
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                    TOPOLOGY:
                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 GGAGGCGGCGGCGGCGGCGGCGG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
 88
                         53 GGAGGCGGCGGCGGCGGCGGCGG 78
                                                 26;
                                                                                                                                                                              nucleic acid
GGAGGCGGCGGCGGCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
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                                                  Conservative
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                                                                                                                              SdC
                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                     UMBER: GB 9709920.4
15-MAY-1997
                                                                                                                                                                single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription Factor Islet-Brain 1 (IB1)
                                                             2.0%;
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                                                               Score 26; Pred. No.
                                                                                                                                                                                                                                  ME A9702
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Pred. No.
                                                    Mismatches
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 63
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                                                                            DB 2;
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                                                                                                                                                                                                                                                                                                                                                                  RESULT 46
                             Sequence 7, Application US/09575081B
Patent NO. 6692934
GENERAL INFORMATION:
APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
TITLE OF INVENTION: NOVEL ORGANIC ANION TRANSPORT PROTEINS
FILE REFERENCE: DB23
CURRENT APPLICATION NUMBER: US/09/575,081B
CURRENT FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
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SEQ ID NO 1858
LENGTH: 2994
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEO ID NOS: 207012
PRIOR SECULOR OF SECUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-949-016-1858
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: GB9706731.8 PRIOR FILING DATE: 1997-04-03 PRIOR APPLICATION NUMBER: GB970920.4
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CURRENT FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: PCT/GB98/00972
PRIOR FILING DATE: 1998-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
PRIOR APPLICATION NUMBER: 60/135,081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2953
TYPE: DNA
ORGANISM: rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 GGAGGCGGCGGCGGCGGCGGCGG 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 GAGGAGGCGGCGGCGGCGGC 76
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SJK/FP5805569
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100.0%; Pred. No.
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Pred. No.
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0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2994;
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374 GGCGGCGGCGGCGGCGGCGAGG 399

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2397)..(2397)
; OTHER INFORMATION: k = g or
US-09-575-081B-7
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US-09-799-451-260
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                                                                                    US-09-799-451-260
                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt FL genes Version 2.0
SEQ ID NO 260
SEQ ID NO 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 260, Application US/09799451 Patent No. 6783969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
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                           Matches
                                          Best Local Similarity
                                                    Query Match
                                                                                               LENGTH: 3725
TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (718)...(2778)
                                                                                                                                                                                                                                                       APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc feature
LOCATION: (713)...(713)
OTHER INFORMATION: y = c
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TYPE: DNA
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56 GGCGGCGGCGGCGGCGGAGG 81
                           26;
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Goodrich, Ryle
Asundi, Vinod
                                                                                                                                                                                                                                                                                                                     Wehrman, Tom
Ghosh, Reena
                                                                                                                                                                                                                                                                                                                                                                                                           Ma, Yunqing
Yamazaki, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao, Qing A.
Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang, Jie
Xue, Aidong J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                 Yang, Yonghong
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                           Conservative
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                                          Score 26; DB 3; ; Pred. No. 0.13;
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Pred. No.
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                            Mismatches
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0.13;
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                                                       Length 3725;
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US-10-104-047-1017
Sequence 1017, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
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US-09-949-016-5656
                                                                                      RESULT 50
US-09-949-016-1137
; Sequence 1137, Application US/09949016
; Patent No. 6812339
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US-10-104-047-1017
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LENGTH: 4412
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APPLICANT: VENTER, J.
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
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                 APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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ORGANISM: Human
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ILE REFERENCE: CL001307
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-09-08
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 197
                                  51 GAGGAGGCGGCGGCGGCGGCGGC 76
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 GAGGAGGCGGCGGCGGCGGCGGC 222
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APPLICANT: Lee, Richard T.

APPLICANT: Landschulz, Katherine T.

APPLICANT: Turi, Thomas G.

APPLICANT: Thompson, John F.

APPLICANT: Kennedy, Scot F.

APPLICANT: Kennedy, Scot F.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS FILE REFERENCE: P0738/7001/ERP/KA

CURRENT APPLICATION NUMBER: US/09/934,249

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 60/227,159

PRIOR PILING DATE: 2000-08-22

NUMBER OF ESO ID NOS: 17

SOFTWARE: FASTSEQ for Windows Version 3.0

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APPLICANT: Hillan, Kenneth
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
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Publication No. US20030148408A1
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CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
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                Sequence 84, Application US/10269909
Publication No. US20030180747A1
GENERAL INFORMATION:
APPLICANT: HRUBAN, RALPH H.
APPLICANT: ARGANI, PEDRAM
APPLICANT: IACOBUZIO-DONAHUE, CHRI
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CURRENT APPLICATION NUMBER: US/10/269,909
CURRENT FILING DATE: 2003-10-11
PRIOR APPLICATION NUMBER: 60/328,609
PRIOR FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 60/322,754
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
SOFTWARE: PATENTIN NUMBER: 60/332,754
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	Query Match 93.0%; Score 1229; DB 6; Length 4839; Best Local Similarity 100.0%; Pred. No. 0; Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  OV 93 GGAAAGCTAGCGGCAGAGGCTCAGCCCCGGCGGCGCGGC	; NUMBER OF SEQ ID NOS: 87 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 85 ; LENGTH: 4839 ; TYPE: DNA ; ORGANISM: Homo sapiens		IACOBUZI MAITRA, NVENTION: ENCE: 583	; Publication No. US20030180747A1 ; GENERAL INFORMATION: ; APPLICANT: HRUBAN, RALPH H. ; APPLICANT: ARGANI, PEDRAM	RESULT 4 US-10-269-909-85 ; Sequence 85, Application US/10269909	Qy 1293 GGGCTGGGGTCGTAAGTGAAAAGGCAG 1321	OY 1233 TCTGGAGCAAAGGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGCC 1292						781 ACGGGAAGCCCCCACCCTACCAAGGCCCCTGCACCTCCAGCTTCGGGACCCCGAGC
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US-10-872-972-119

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APPLICANT: FITATICS,
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TREATMENT OF TUMOR
TILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/872,972
CURRENT APPLICATION NUMBER: US/10/241,220
PRIOR APPLICATION NUMBER: US/10/241,220
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 120
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100.0%; Pred. No.
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; ORGANISM: Homo Sapien US-10-872-991-119

Query Match Best Local Similarity Matches 1229; Conserv

93.0%; Score 1229; 1 ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches

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                                                                                                                                                                                                                                Sequence 119, Application US/10872991
Publication No. US20040242860A1
GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
              SEQ ID NO 119
LENGTH: 4839
                                        APPLICANT: Zhang,Zemin

APPLICANT: Zhang,Zemin

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: TREATMENT OF TUMOR

FILE REFERENCE: P5010R1-US

CURRENT APPLICATION NUMBER: US/10/872,991

CURRENT FILING DATE: 2004-06-21

PRIOR APPLICATION NUMBER: US/10/241,220

PRIOR FILING DATE: 2002-09-11

NUMBER: OF SEQ ID NOS: 120
                                                                                                                                                                                                    APPLICANT:
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LENGTH: 48
TYPE: DNA
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Williams, P.Mickey
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US-10-287-436A-300
; Sequence 300, Application US/10287436A
; Publication No. US20050202421A1
; Publication No. US20050202421A1
; GENERAL INFORMATION:
APPLICANT: CHILDEN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREJ
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILLING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 300
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-287-436A-300
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Best Local Similarity 100.0%;
Matches 1229; Conservative
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                                              CCGCCGGGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCA
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APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT TILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: WS 09/663,733
PRIOR APPLICATION NUMBER: WS 09/666
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-10-295-027-127
                                                                                                                                                                                                                                                                                                                                                   Sequence 127, Application US/10295027 Publication No. US20030232350A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR APPLICATION NUMBER: US 60/347,376
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,241
PRIOR PRILING DATE: 2002-01-06
PRIOR FILING DATE: 2002-01-06
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-06
PRIOR FILING DATE: 2002-01-06
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR PILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 127
LENGTH: 864
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                           AGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGGCGCCACGTGCTACGGC 1072
                                                                                    GAGTCGGTGCGCGCCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCC
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LENGTH: 861
TYPE: DNA
ORGANISM: Homo S
FEATURE:
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Patent No. US20020115081A1
GENERAL INFORMATION:
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Best Local
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APPLICANT:
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PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
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                     AGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGAGCACAGTGTCA 712
                                                                                                                                               CTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGGCGG
                                                                                                                                                                            TTTGTTCAGATCATCATCATCGTGGTGATGATGGTGATGGTGGTGATCACGTGC 180
                                                                                                                   AGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCA
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US-10-390-045-1
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PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10390045 Publication No. US20030170713A1 GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 800; Conserv
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APPLICANT: SEGAMA, TAKEHIKO
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
FILE REFERENCE: 04995.0057-00000
CURRENT APPLICATION NUMBER: US/10/390,045
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US/09/769,482
PRIOR APPLICATION NUMBER: US/09/769,482
PRIOR APPLICATION NUMBER: 60/178,772
PRIOR PILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,772
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-26
PRIOR FILING DATE: 2000-01-26
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APPLICANT: MOUL, JUDD W.
APPLICANT: XU, LINDA L.
                                                                                                      ORGANISM: HOMO FEATURE:
NAME/KEY: CDS
LOCATION: (95).
                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                   LENGTH: 1140
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                                                                                                          (95)..(850)
    60.6%; Score 800; DI
100.0%; Pred. No. 0;
rative 0; Mismatches
                                               DB 6; Length 1140;
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RESULT 11

US-10-434-479-1

Sequence 1, Application US/10434479

Publication No. US20040092469A1

GENERAL INFORMATION:
APPLICANT: KOLL, JUDD W.

APPLICANT: WOUL, JUDD W.

APPLICANT: XU, LINDA L.

TITLE OF INVENTION: ANDROGEN-REGULATED PMEPA1 GENE AND FILE REFERENCE: 04995.0057-02000

CURRENT APPLICATION NUMBER: US/10/434,479

CURRENT FILING DATE: 2003-03-18

PRIOR APPLICATION NUMBER: 10/390,045

PRIOR APPLICATION NUMBER: 09/769,482

PRIOR APPLICATION NUMBER: 09/769,482

PRIOR FILING DATE: 2001-01-26
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PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 81
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1140
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: CDS
ICCATION: (95)..(850)
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                                             AAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCGGGCTGGGG
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; SEQ ID NO 412
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-412
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CURRENT FILING DATE: 2002-07-25
CURRENT FILICATION NUMBER: 60/307,982
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schlegel, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/362,158
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FILING DATE: 2001-09-25
APPLICATION NUMBER: 60/341,746
FILING DATE: 2001-12-12
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AGCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCAGCTGG 941
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Gorbatcheva, Bella
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Kamatkar, Shubhangi
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Endege, Wilson O.
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PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF COM-
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LENGTH: 114
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APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: MPMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
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                                                                                 NAME/KEY: CDS
LOCATION: (96
                                                                                                                                ORGANISM: Homo
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Schlegel, Robert
Monahan, John E.
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 60.6%; Score 800; Dilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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US-11-051454-412

Sequence 412, Application US/11051454

Publication No. US20050191673A1

GENERAL INFORMATION:
APPLICANT: Schlegel, Robert

APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Wonsey, Angela M.
APPLICANT: Glatt, Karen

APPLICANT: Glatt, Karen

APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
                                                                                                                                                                                                                                                                                                                                                 RESULT 14
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PRIOR APPLICATION NUMBER: US/11/051,454
CURRENT FILING DATE: 2005-02-04
PRIOR APPLICATION NUMBER: US/10/205,823
PRIOR FILING DATE: 2002-07-25
PRIOR PILING DATE: 2001-07-25
PRIOR PILING DATE: 2001-07-25
PRIOR PILING DATE: 2001-08-22
PRIOR PILING DATE: 2001-08-22
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR PILING DATE: 2001-12-12
PRIOR PILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 412
LENGTH: 1141
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; LENGTH: 1850
; TYPE: DNA
; TYPE: DNA
; ORGANISM: Homo Sapien
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Publication No.
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
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Hillan, Kenneth J.
Phillips, Heidi
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                          AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 1001
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No. US20030148408A1
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Williams, P.Mickey
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Best Local Similarity
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TYPE: DNA
ORGANISM: Homo Sapien
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  ACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCT 821
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                                                                                   LENGTH: 1850
TYPE: DNA
ORGANISM: Homo S
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Matches 800
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                                                                                                                           APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS I
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/872,991
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/10/241,220
RIOR APPLICATION STATE CONTROL OF SERVING DATE: 2002-09-11
NUMBER OF SERVINGS: 120
                                                                                                                                                                                                             APPLICANT:
                                                                            -10-872-991-44
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APPLICANT: Hillan, Kenneth
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
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Williams, P.Mickey
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                                 60.6%; Score 800; DB ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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Sequence 2, Application US/09821812
Publication No. US20030166520A1
GENERAL INFORMATION:
APPLICANT: Lin, Biaoyang
ITITLE OF INVENTION: Androgen Regulated Prostate Spe
ITITLE OF INVENTION: Nucleic Acids
FILE REFERENCE: P-1S 4373
CURRENT APPLICATION NUMBER: US/09/821,812
CURRENT FILING DATE: 2001-03-28
INUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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RESULT 19
US-10-849-635-2
(Sequence 2, Application US/10849635
; Dublication No. US20040253622A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Biaoyang
; TITLE OF INVENTION: Androgen Regulated
; TITLE OF INVENTION: Nucleic Acids
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CURRENT APPLICATION NUMBER: US/10/849,635
CURRENT FILING DATE: 2004-05-19
PRIOR APPLICATION NUMBER: US/09/821,812
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 11
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
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APPLICANT: Zhang, Jie
APPLICANT: Qian, Xiaohong B.
APPLICANT: Qian, Xiaohong B.
APPLICANT: Qian, Xiaohong B.
APPLICANT: Dynamac, Radoje T.
TITLE OF INVENTION: NO. US20020197679A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CTP2
CURRENT APPLICATION NUMBER: US/10/098,841
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/552,317
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; LOCATION: (154)..(867)
US-10-098-841-71
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Aundi, Chongjun
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunqing
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SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 71
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Best Local Similarity
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                                                                                                                                      GGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAG
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Wang, Zhiwei
Wehrman, Tom
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Chen, Rui-hong
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Zhao, Qing A.
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GENERAL INFORMATION:
APPLICANT: SRIVASTAVA, SHIV
APPLICANT: SRIVASTAVA, SHIV
APPLICANT: SRIVASTAVA, SHIV
APPLICANT: XU, LINDA L.
APPLICANT: XU, LINDA L.
APPLICANT: SEGAMA, TAKEHIKO
ITITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
ITITLE OF INVENTION: POYNUCLEOTIDE ARRAY
ITITLE OF INVENTION: POYNUCLEOTIDE ARRAY
ITITLE OF INVENTION: US/10/300,045
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US/09/769,482
PRIOR APPLICATION NUMBER: 60/178,772
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
COURTAINED: TOTALTON TOTA
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-390-045-2
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SEQ ID NO 2
LENGTH: 759
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                                                                                                                                                                                                                                                                                            Query Match
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                                                                          PRIOR APPLICATION NUMBER: 10/390,045
PRIOR FILING DATE: 2003-03-18
PRIOR PELICATION NUMBER: 09/769,482
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,772
PRIOR FILING DATE: 2000-01-28
PRIOR PELICATION NUMBER: 60/179,045
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 81
                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10434479 Publication No. US20040092469A1 GENERAL INFORMATION:
                              SEQ ID NO 2
LENGTH: 759
                                                                                                                                                                                                                           APPLICANT: SRIVASTAVA, SHIV
APPLICANT: MOUL, JUDD W.
APPLICANT: XU, LINDA L.
TITLE OF INVENTION: ANDROGEN-REGULATED PMF
FILE REFERENCE: 04995,0057-02000
CURRENT APPLICATION NUMBER: US/10/434,479
CURRENT FILING DATE: 2003-05-09
                                                               SOFTWARE: PatentIn Ver.
ORGANISM: Homo sapiens
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 CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
                                                                                                    APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
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; NAME/KEY: CDS
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US-09-796-753-55
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Best Local Similarity
Matches 799; Conserv
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LENGTH: 969
TYPE: DNA
ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
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OR FILING DATE: 1999-12-23
OR APPLICATION NUMBER: 09/474,071
OR FILING DATE: 1999-12-29
OR APPLICATION NUMBER: 09/474,072
OR APPLICATION NUMBER: 09/474,072
OR APPLICATION NUMBER: 09/514,010
OR FILING DATE: 2000-02-25
OR APPLICATION NUMBER: 09/516,745
OR APPLICATION NUMBER: 09/516,745
OR APPLICATION NUMBER: 09/572,002
OR FILING DATE: 2000-05-14
OR PILING DATE: 2000-05-14
OR PILING DATE: 2000-05-07
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R FILING DATE: 2000-0
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R APPLICATION NUMBER:
R FILING DATE: 1999-06
R FILING DATE: 1999-07
R FILING DATE: 1999-07
R APPLICATION NUMBER:
R FILING DATE: 1999-09
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R APPLICATION NUMBER:
R FILING DATE: 1999-06
R APPLICATION NUMBER:
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APPLICATION NUMBER: 09/606,317
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APPLICATION NUMBER:
FILING DATE: 1999-
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nilarity 99.9%;
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Pred. No. 0;
0; Mismatches
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Query Match Best Local Similarity

54.0%;

Score Pred.

13; No. 0; BB

Length

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; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo 9
US-10-241-220-45
                                                                                                                                                                                                                                    Sequence 45, Application US/10241220
Publication No. US20030148408A1
GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams p Micher.
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                                                                   NUMBER OF SEQ ID NOS:
SEQ ID NO 45
                                                                                                   APPLICANT: WU, Thomas
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
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Spencer, Susan
Williams, P.Mickey
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GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J
APPLICANT: Hillian, Heidi
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Micke
APPLICANT: Wu, Thomas
                                                                                                                                                                                                                                RESULT 25
US-10-872-972-45
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/872,972
CURRENT FILING DATE: 2004-06-21
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Best Local Similarity
Matches 763; Conserv
 Sequence 45, Application US/10872991
Publication No. US20040242860A1
GENERAL INFORMATION:
APPLICANT: Frantz,Gretchen
APPLICANT: Hillan,Kenneth J.
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APPLICANT: Wu, Thomas
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TREATMENT OF TUMOR
TITLE OF INVENTION: TREATMENT OF TUMOR
TILE REPERENCE: PSOIORI-US
CURRENT APPLICATION NUMBER: US/10/872,991
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/10/241,220
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 45
LENGTH: 806
TYPE: DNA
ORGANISM: Homo Sapien
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Similarity 99.9%;
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                                                 AGGGGACCCGGCTCCACCACACACACACCGCCCCTAGAGAGCCGCAGCCATCTGGAGCA 1241
                                                                                             GCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGCAGTGGGCCGCCCTCCTTGCTGG
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                                AGGGGACCCGGCTCCACCACACACACACCCCCCCCTAGAGAGCGCAGCCATCTGGAGCA
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Polakis, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 713;
Pred. No. 0;
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CURRENT APPLICATION NUMBER: US/10/000,256A
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION UNMBER: 60/244,782
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 1583
TYPE: DNA
ORGANISM: Homo sapien
US-10-000-256A-32
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Publication No. US20030039983A1
GENERAL INFORMATION:
APPLICANT: Sun, Yongming
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
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Best Local Similarity
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APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to
FILE REFERENCE: DEX-0259
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                   TCTCTAGGGTCCCCAGGGGG 1289
                                                            CGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCC
                                                                            CGCGCCCCTAGAGAGAGCGCAGCCATCTGGAGCAAAGAGAAAGGATAAACAGAAAGGACACCC
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 TCTCTAGGGTCCCCAGGGGG
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100.0%; Pred. No. 1.4e-265;
vative 0; Mismatches 0;
1386
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RESULT

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SEQ ID NO 11658
LENGTH: 408
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Best Local Similarity
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CURRENT FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: 10/076,555
PRIOR FILING DATE: 2002-02-15
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FILING DATE: 1998-12-21
APPLICATION NUMBER: 60/068,755
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APPLICATION NUMBER: 60/072,910
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                                                                                                                                                           TCCGTACCTGCAGCACGAGATCGACCTGCCACCATCTCGCTGTCAGACGGGGAGGA
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                                      ACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCA 983
                                                                               GCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGA
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100.0%; Pred. No. 4.3e-187;
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SEQ ID NO 14
LENGTH: 693
                                                                                                                                                                                                           Sequence 2074, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 302; Conserv
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SEQ ID NO 2074
                                                APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR FILING DATE: 1999-01-20
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
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                    NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
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NAME/KEY: unsure
LOCATION: (639)...(639)
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ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 100.0%; Conservative 0;
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US-09-783-590-3464; Sequence 3464, Application US/09783590; Patent No. US20020110850A1
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US-10-450-763-20307
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SOFTWARE: Custom
SEQ ID NO 20307
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Best Local S
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                                                                                                                                                                                                                                                                                                                        Query Match
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SIMILAR
LOCATION: (473)..(835)
COTHER INFORMATION: 32% homologous to Homo sapiens dJ718J7.1 (PMEPA1 protein (an OTHER INFORMATION: androgen induced type 1b transmembrane protein).),accession numb
OTHER INFORMATION: AL035541,Smith-Waterman Score=95.
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NAME/KEY: misc_feature
LOCATION: (1)...(467)
OTHER INFORMATION: n = A,T,C
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TYPE: DNA
ORGANISM: Homo sapiens
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Conservative 0;
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                                                                                                                                                                                                                                                                                                    8.0%; Score 106; DB 9;
100.0%; Pred. No. 1e-41;
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TITLE OF INVENTION: Human Genes, Sequences, an FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR PILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3464
LENGTH: 368
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US-10-450-763-20306
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GENERAL INFORMATION:
APPLICANT: HYSEQ, IIC
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
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                                                                                                          Sequence 20306, Application US/10450763 Publication No. US20050196754A1
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Best Local Similarity
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APPLICANT: Haseltine, William
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
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LOCATION: (368)
OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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LOCATION: (103)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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LOCATION: (314)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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Ruben, Steven M.
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Pred. No. 1.2e-39;
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                                                                                               Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                            SEQ ID NO 13620
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Publication No. US20030165843A1
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                                                                                                                                                             -09-908-975-13620
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CURRENT FILING DATE: 2001-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FAIGLER, SIMCHON
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
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PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/287,724 PRIOR FILING DATE: 2001-05-02
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                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/221,607
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LOCATION: (1)...(426)
OTHER INFORMATION: n = a,t,c or
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OTHER INFORMATION: 93% homologous to Homo sapiens dJ718J7.1 (PMEPA1 protein OTHER INFORMATION: androgen induced type 1b transmembrane protein).),accessi OTHER INFORMATION: AL035541,Smith-Waterman Score=79.
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                                                                                                                                                                                                                                                               PatentIn version
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  CGCAGCCATCTGGAGCAAAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCA 60
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MINTZ, Liat
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Pred. No.
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2e-20;
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US-10-240-425-166
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                                                                              US-09-783-590-3488
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LENGTH: 522
TYPE: DNA
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                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. SEQ ID NO 3488
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Matches
                  Best Local Similarity
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Patent No. US20020110850Al
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CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR APPLICATION NUMBER: US 60/193,446
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APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
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NUMBER OF SEQ ID NOS: 1588
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences,
FILE REFERENCE: PO-16.2C1
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                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/783,590 CURRENT FILING DATE: 2000-02-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT: Vockley, Joseph G.
TILE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
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                                                                                               OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                    NAME/KEY: misc feature LOCATION: (51)
                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                     ENGTH: 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li, Haodong
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  Conservative
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100.0%; Pred. No.
                    3.8%; Score 50; DB 3;
100.0%; Pred. No. 7e-14;
    Mismatches
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                                         Length 65;
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US-10-363-483A-30091
; Sequence 30091, Application US/10363483A
; Publication No. US20050064401A1
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US-10-363-345A-30091
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                                                                 RESULT 39
                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens); OTHER INFORMATION: CpG-island No: 30092
US-10-363-345A-30092
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Method for determining the degree of methylation of defined TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3 FILE REFERENCE: E01/127 CURRENT APPLICATION NUMBER: US/10/363,345A CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 30092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 30091
LENGTH: 837
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APPLICANT: Christian Piep
APPLICANT: Kurt Berlin
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Kurt Berlin
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                                                                                                                                                                     TTGAATGAGGAGGAGGAGGCGCCGCCGCCGCCGCCGAGGCG 83
                                                                                                                                                                                                            3.4%; Score 45; DB 8; ilarity 100.0%; Pred. No. 1.4e-1 Conservative 0; Mismatches
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100.0%; Pred. No. 1.
ive 0; Mismatches
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hes 0;
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US-10-363-483A-30092/c
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US-09-934-249-12
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CURRENT APPLICATION NUMBER: US/10/363,483A

CURRENT FILING DATE: 2003-03-03

NUMBER OF SEQ ID NOS: 40712

SEQ ID NO 3092
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FILE REFERENCE: 82011
CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 30091
LENGTH: 837
TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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                                                                                                                                                                               Sequence 12, Application US/09934249 Patent No. US20020115081A1
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                                                          APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine
APPLICANT: Turi, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnesses
TITLE OF INVENTION: illnesses
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APPLICANT: Christian Pier
APPLICANT: Kurt Berlin
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDITOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) OTHER INFORMATION: CpG-island No: 30092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 837
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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Pred. No. 1.4e-11;
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RESULT 42
US-09-796-753-57
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; NAME/KEY: CDS
; LOCATION: (20)...(841)
US-09-934-249-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 57, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
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ORGANISM: Mus Musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-1 APPLICATION NUMBER:
                                                                                                          APPLICATION NUMBER: 09/474,071 FILING DATE: 1999-12-29 APPLICATION NUMBER: 09/474,072
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 1999-0
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                                                                                                                                                                             APPLICATION NUMBER: 09/471,179
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l Similarity 100.0%; Pred. No.
44; Conservative 0; Mismatch
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               CATION NUMBER:
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VENTION: SECRETED PROTEINS AND USES THEREOF
NCE: 7853-227-999
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               09/572,002
                                                09/516,745
                                                                             09/514,010
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RESULT 44
US-10-363-345A-30089/c
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                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Mus Musculus
US-09-934-249-15
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US-09-934-249-15
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LENGTH: 1713
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS FILE REFERENCE: 90738/7001/ERP/KA CURRENT APPLICATION NUMBER: US/09/934,249 CURRENT FILING DATE: 2001-08-21 PRIOR APPLICATION NUMBER: US 60/227,159 PRIOR FILING DATE: 2000-08-22
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LOCATION: (2)...(652)
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                                                                                                                                                                                                                                        LENGTH: 475
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                                                                                             438 GCACCGCCGCCGCCGCCGGCCAGCCCAATGTCTCCTGC 478
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                                                               33 GCACCGCCGCCGCCGCCGGCAGCCCAATGTCTCCTGC 73
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                                                                                                                                                                                                                                                                                                                                                                                                                   Thompson, John F. Kennedy, Scott P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Turi, Thomas
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                                                                                                                            ilarity 100.0%;
Conservative
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100.0%; Pred. No. 3.8e-11;
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; Pred. No. 1.4e-09
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                                                                                                                                 Mismatches
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Sequence 30089, Application US/10363345A Publication No. US20040234960A1

GENERAL

INFORMATION

Christian Piepenbrock

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                                                                                                                                                                                                                                                                                          RESULT 46
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically to
OTHER INFORMATION: CPG-island
CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 30089
                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                              Sequence 30089, Application US/10363483A Publication No. US20050064401A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-
TILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Method for determining the degree of methylation of defined TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3 FILE REFERENCE: E01/1227
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CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
                                                                             TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain TITLE OF INVENTION: illnesses
                                                                                                                                          APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 837
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) OTHER INFORMATION: CpG-island No: 30090
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 8; ; Pred. No. 1.2e-0
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; Pred. No. 1.2e-C
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        ٥,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 48
US-10-425-115-66221
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                                                                                                                                              FILE REFERENCE: 38-21(53222)B CURRENT APPLICATION NUMBER: US/10/425,115 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 369326 SEQ ID NO 66221 LENGTH: 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 30090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 66221, Application US/10425115 Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acid Molecules
                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain TITLE OF INVENTION: illnesses
FILE REFERENCE: 82011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: CpG-island No: 30090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                     NAME/KEY: unsure
LOCATION: (1)..(555)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_160394C.1
                                                                                              FEATURE:
                                                                                                            ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 837
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nes 37; Conserv
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Conservative
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Pred. No. 1.2e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treated genomic DNA (Homo sapiens) No: 30089
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; OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER54078_1
US-10-739-930-3690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-739-930-3690/c
                                                                        Query Match
Best Local S
Matches 34
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SEQ ID NO 146
LENGTH: 640
TYPE: DNA
ORGANISM: Eucalyptus grandis
3-10-856-499-146
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 3690
SEQ ID NO 3690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 146, Application US/10856499
Publication No. US20040259145A1
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Best Local Similarity
Matches 34; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/856,499
CURRENT FILING DATE: 2004-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Modification of Gene Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 2370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wood, Marion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                    ENGTH: 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 GAGGAGGAGGCGGCGGCGGCGGCGGCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 GAGGAGGAGGCGGCGGCGGCGGCGGCGGCGG
  422 GAGGAGGAGGCGGCGGCGGCGGCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 GAGGAGGAGGCGGCGGCGGCGGCGGCGGCGG
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                                      45 GAGGAGGAGGAGGCGGCGGCGGCGGCGGCGG
                                                                                              Similarity
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McGrath, Annette
Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.6%; Score 34; DB 8; Liarity 100.0%; Pred. No. 3.8e-06; Conservative 0; Mismatches 0;
                                                                        2.6%; Score 34; DB 8; Local Larity 100.0%; Pred. No. 3.5e-06; Conservative 0; Mismatches 0;
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Minimum DB
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US-10-310-914A-7162

US-11-072-512-70

US-11-12-944-14

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2 US-11-121-086-14

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14 US-11-124-367A-23496
15 US-11-124-367A-23496
16 US-11-124-367A-23496
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18 US-10-310-914A-2051
18 US-11-124-367A-206
19 US-11-124-367A-207
19 US-11-124-367A-207
10 US-11-124-367A-207
11 US-11-124-367A-209
12 US-11-124-367A-209
13 US-10-310-914A-2051
14 US-11-124-367A-209
15 US-10-310-914A-2051
16 US-10-310-914A-2051
17 US-11-136-527-252
18 US-10-310-914A-2051
18 US-10-310-914A-2051
19 US-11-043-752-373
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RESULT 1  US-11-186-284-208  US-11-186-284-208  DUS-11-186-284-208  Publication No. US20  GENERAL INFORMATION  APPLICANT: Millenni APPLICANT: Millenni APPLICANT: Schlege  APPLICANT: Kamatka  APPLICANT: Wonahan  APPLICANT: Honahan  APPLICANT: Honahan  APPLICANT: Honahan  APPLICANT: Honahan  APPLICANT: Honahan  APPLICANTI HILDON  TITLE OF INVENTION  TITLE OF INVENTION  TITLE OF INVENTION  TILE REFERENCE: MPPLICATION  FILE REFERENCE: MPPLICATION  FILE REFLICATION  FRIOR FILING DATE:  PRIOR APPLICATION  PRIOR APPLICATION  PRIOR APPLICATION  PRIOR APPLICATION  PRIOR FILING DATE:		348 23 1.7 349 23 1.7 350 23 1.7 351 23 1.7	344 23 1.7 345 23 1.7 346 23 1.7 347 23 1.7	341 23 1.7 342 23 1.7 343 23 1.7	23 1.7 23 1.7 23 1.7	335 23 1.7 336 23 1.7 337 23 1.7	333 23 1.7 334 23 1.7	331 23 1.7 332 23 1.7	328 23 1.7 329 23 1.7 330 23 1.7	326 23 1.7 327 23 1.7	324 23 1.7 325 23 1.7	322 23 1.7 323 23 1.7	319 23 1.7 320 23 1.7 321 33 1 7	317 23 1.7 318 23 1.7	314 23 1.7 315 23 1.7 316 23 1.7	313 23 1.7
RESULT 1  US-11-186-284-208  US-11-186-284-208  Sequence 208, Application publication No. US20050266  GENERAL INFORMATION:  APPLICANT: Millennium ph.  APPLICANT: Guillemette, Guillemette, APPLICANT: Kamatkar, Sh.  APPLICANT: Monahan, Joh.  APPLICANT: Monahan, Joh.  APPLICANT: Morahan, Joh.  APPLICANT: MOUSTION: MOVE.  TITLE OF INVENTION: MOVE.  TITLE OF INVENTION: MET.  TITLE OF INVENTION: MUMB.  CURRENT APPLICATION NUMBER.  PRIOR APPLICATION NUMBER.  PRIOR APPLICATION NUMBER.  PRIOR APPLICATION NUMBER.  PRIOR FILING DATE: 2001-  PRIOR APPLICATION NUMBER.  PRIOR FILING DATE: 2002-  NUMBER OF SEQ ID NOS: 22  SOFTWARE: FastSEQ for Willing DATE: 2001-		348 23 1.7 349 23 1.7 350 23 1.7 351 23 1.7	344 23 1.7 345 23 1.7 346 23 1.7 347 23 1.7	341 23 1.7 342 23 1.7 343 23 1.7	23 1.7 23 1.7 23 1.7	335 23 1.7 336 23 1.7 337 23 1.7	333 23 1.7 334 23 1.7	331 23 1.7 332 23 1.7	328 23 1.7 329 23 1.7 330 23 1.7	326 23 1.7 327 23 1.7	324 23 1.7 325 23 1.7	322 23 1.7 323 23 1.7	319 23 1.7 320 23 1.7 321 33 1 7	317 23 1.7 318 23 1.7	314 23 1.7 315 23 1.7 316 23 1.7	313 23 1.7
RESULT 1  US-11-186-284-208  US-11-186-284-208  JEQUENCE 208, Application US/J  Publication No. US20050266493J  GENERAL INFORMATION:  APPLICANT: Millennium Pharmac  APPLICANT: Millenette, Trac  APPLICANT: Genilemette, Trac  APPLICANT: Schlegel, Robert  APPLICANT: Kamatkar, Shubhar  APPLICANT: Monahan, John B.  APPLICANT: Hibodeau, Stephc  APPLICANT: Hibodeau, Stephc  APPLICANT: HIPOTION: WETHODS  TITLE OF INVENTION: WETHODS  TITLE OF INVENTION: WETHODS  TITLE OF INVENTION UNMBER: US  PRIOR APPLICATION NUMBER: US  PRIOR FILING DATE: 2002-03-03  PRIOR FILING DATE: 2002-03-05  PRIOR FILING DATE: 2002-05-20  NUMBER OF SEQ ID NOS: 228  SOFTWARE: FastSEQ for Window		348 23 1.7 170189 1 349 23 1.7 170285 1 350 23 1.7 172543 1 351 23 1.7 193789 1	344 23 1.7 150466 1 345 23 1.7 157224 1 346 23 1.7 164810 1 347 23 1.7 168656 1	341 23 1.7 34875 8 342 23 1.7 63693 8 343 23 1.7 139054 1	23 1.7 7006 8 23 1.7 11564 1 23 1.7 12277 8	335 23 1.7 5614 1 336 23 1.7 5727 1 337 23 1.7 5727 1	333 23 1.7 5011 7 334 23 1.7 5011 1	331 23 1.7 4677 8 332 23 1.7 4982 8	328 23 1.7 4314 7 329 23 1.7 4457 1 330 23 1.7 4642 1	326 23 1.7 4275 1 327 23 1.7 4290 1	324 23 1.7 3337 1 325 23 1.7 3958 1	322 23 1.7 3167 6 323 23 1.7 3293 8	319 23 1.7 3108 8 320 23 1.7 3147 8 321 23 1 7 3158 9	317 23 1.7 3073 1 318 23 1.7 3081 8	314 23 1.7 2805 1 315 23 1.7 2954 1 316 23 1.7 3050 1	313 23 1.7 2690
RESULT 1  US-11-186-284-208  (Sequence 208, Application US/11186)  Publication No. US20050266493A1  GENERAL INFORMATION:  APPLICANT: Millennium Pharmaceuti APPLICANT: Millennium Pharmaceuti APPLICANT: Genilemette, Tracy L. APPLICANT: Kamatkar, Shubhangi APPLICANT: Kamatkar, Shubhangi APPLICANT: Honahan, John E. APPLICANT: Honahan, John E. APPLICANT: Hibodeau, Stephen N. APPLICANT: Thibodeau, Stephen N. APPLICANT: Thibodeau, Stephen N. APPLICANT: Honahan, John E. TITLE OF INVENTION: METHODS FOR TITLE OF INVENTION: METHODS FOR TITLE OF INVENTION: METHODS FOR TITLE OF INVENTION UMBER: US/11 CURRENT APPLICATION NUMBER: US/11 CURRENT FILING DATE: 2005-07-21 PRIOR APPLICATION NUMBER: US/11 PRIOR APPLICATION NUMBER: US/10/3 PRIOR APPLICATION NUMBER: US 60/3 PRIOR FILING DATE: 2001-12-10 PRIOR APPLICATION NUMBER: US 60/3 PRIOR FILING DATE: 2002-03-05 PRIOR FILING DATE: 2002-05-20 NUMBER OF SEQ ID NOS: 228 SOFTWARE: FastSEQ for Windows Ver		348 23 1.7 170189 1 349 23 1.7 170285 1 350 23 1.7 172543 1 351 23 1.7 193789 1	344 23 1.7 150466 1 345 23 1.7 157224 1 346 23 1.7 164810 1 347 23 1.7 168656 1	341 23 1.7 34875 8 342 23 1.7 63693 8 343 23 1.7 139054 1	23 1.7 7006 8 23 1.7 11564 1 23 1.7 12277 8	335 23 1.7 5614 1 336 23 1.7 5727 1 337 23 1.7 5727 1	333 23 1.7 5011 7 334 23 1.7 5011 1	331 23 1.7 4677 8 332 23 1.7 4982 8	328 23 1.7 4314 7 329 23 1.7 4457 1 330 23 1.7 4642 1	326 23 1.7 4275 1 327 23 1.7 4290 1	324 23 1.7 3337 1 325 23 1.7 3958 1	322 23 1.7 3167 6 323 23 1.7 3293 8	319 23 1.7 3108 8 320 23 1.7 3147 8 321 23 1 7 3158 9	317 23 1.7 3073 1 318 23 1.7 3081 8	314 23 1.7 2805 1 315 23 1.7 2954 1 316 23 1.7 3050 1	313 23 1.7 2690 9
RESULT 1  US-11-186-284-208  US-11-186-284-208  Sequence 208, Application US/11186284  Publication No. US20050266493A1  GENERAL INFORMATION:  APPLICANT: Millennium Pharmaceuticals, APPLICANT: Millemette, Tracy L. APPLICANT: Schlegel, Robert APPLICANT: Monahan, John E. APPLICANT: MOTAHAN, Stephen N. APPLICANT: MITTLE OF INVENTION: METHODS FOR IDENTITLE OF INVENTION UNMER: US/11/186.  CURRENT FILING DATE: 2005-07-21  PRIOR APPLICATION NUMBER: US 60/339,9  PRIOR APPLICATION NUMBER: US 60/339,9  PRIOR APPLICATION NUMBER: US 60/361,9  PRIOR FILING DATE: 2002-03-05  PRIOR APPLICATION NUMBER: US 60/361,9  PRIOR FILING DATE: 2002-05-20  NUMBER OF SEQ ID NOS: 228  SOFTWARE: FastSEQ for Windows Version	ALIGN	348 23 1.7 170189 1 349 23 1.7 170285 1 350 23 1.7 172543 1 351 23 1.7 193789 1	344 23 1.7 150466 1 345 23 1.7 157224 1 346 23 1.7 164810 1 347 23 1.7 168656 1	341 23 1.7 34875 8 342 23 1.7 63693 8 343 23 1.7 139054 1	23 1.7 7006 8 23 1.7 11564 1 23 1.7 12277 8	335 23 1.7 5614 1 336 23 1.7 5727 1 337 23 1.7 5727 1	333 23 1.7 5011 7 334 23 1.7 5011 1	331 23 1.7 4677 8 332 23 1.7 4982 8	328 23 1.7 4314 7 329 23 1.7 4457 1 330 23 1.7 4642 1	326 23 1.7 4275 1 327 23 1.7 4290 1	324 23 1.7 3337 1 325 23 1.7 3958 1	322 23 1.7 3167 6 323 23 1.7 3293 8	319 23 1.7 3108 8 320 23 1.7 3147 8 321 23 1 7 3158 9	317 23 1.7 3073 1 318 23 1.7 3081 8	314 23 1.7 2805 1 315 23 1.7 2954 1 316 23 1.7 3050 1	313 23 1.7 2690 9 US-11-07
RESULT 1  US-11-186-284-208  US-11-186-284-208  Sequence 208, Application US/11186284  Publication No. US20050266493A1  GENERAL INFORMATION:  APPLICANT: Millennium pharmaceuticals, Inc.  APPLICANT: Millennium pharmaceuticals, Inc.  APPLICANT: Guillemette, Tracy L.  APPLICANT: Schlegel, Robert  APPLICANT: Monahan, John E.  APPLICANT: Monahan, John E.  APPLICANT: MONAHAN, John E.  APPLICANT: MOTAHAN, Stephen N.  APPLICANT: MOTAHAN, JOHN E.  APPLICANT: MOTAHAN, JOHN E.  APPLICANT: MOTAHAN, JOHN E.  APPLICANT: MOTAHAN, JOHN E.  APPLICANTION: METHODS FOR COLON-CANC, TITLE OF INVENTION: METHODS FOR COLON CANC, FILE REFERENCE MEMOI-029P2RNM  CURRENT APPLICATION NUMBER: US/11/186,284  CURRENT APPLICATION NUMBER: US 60/339,971  PRIOR APPLICATION NUMBER: US 60/339,971  PRIOR APPLICATION NUMBER: US 60/339,971  PRIOR APPLICATION NUMBER: US 60/361,978  PRIOR APPLICATION NUMBER: US 60/361,988  PRIOR APPLICATION NUMBER: US 60/361,988  PRIOR FILING DATE: 2002-03-05  PRIOR FILING DATE: 2002-05-20  NUMBER OF SEQ ID NOS: 228  SOFTWARE: FastSEQ for Windows Version 4.0	ALIGNMENT	348 23 1.7 170189 1 349 23 1.7 170285 1 350 23 1.7 172543 1 351 23 1.7 193789 1	344 23 1.7 150466 1 345 23 1.7 157224 1 346 23 1.7 164810 1 347 23 1.7 168656 1	341 23 1.7 34875 8 342 23 1.7 63693 8 343 23 1.7 139054 1	23 1.7 7006 8 23 1.7 11564 1 23 1.7 12277 8	335 23 1.7 5614 1 336 23 1.7 5727 1 337 23 1.7 5727 1	333 23 1.7 5011 7 334 23 1.7 5011 1	331 23 1.7 4677 8 332 23 1.7 4982 8	328 23 1.7 4314 7 329 23 1.7 4457 1 330 23 1.7 4642 1	326 23 1.7 4275 1 327 23 1.7 4290 1	324 23 1.7 3337 1 325 23 1.7 3958 1	322 23 1.7 3167 6 323 23 1.7 3293 8	319 23 1.7 3108 8 320 23 1.7 3147 8 321 23 1 7 3158 9	317 23 1.7 3073 1 318 23 1.7 3081 8	314 23 1.7 2805 1 315 23 1.7 2954 1 316 23 1.7 3050 1	313 23 1.7 2690 9 US-11-072-5
RESULT 1  US-11-186-284-208  US-11-186-284-208  JEQUARICA 208  PUBLICANT: MILLENDING PHARMACCULICALS, INC.  APPLICANT: MILLENDING PHARMACCULICALS, INC.  APPLICANT: MILLENDING PHARMACCULICALS, INC.  APPLICANT: Guillemette, Tracy L.  APPLICANT: Guillemette, Tracy L.  APPLICANT: Guillemette, Tracy L.  APPLICANT: Monahan, John E.  APPLICANT: Monahan, John E.  APPLICANT: Burgart, Lawrence J.  APPLICANT: MONAHAN, John E.  APPLICANTION: METHODS FOR IDENTIFICATION, UND FOR IDENTIFICATION TITLE OF INVENTION INTERAPY OF COLON CANCER FILL REFERENCE: MEMOI-029P2NM  CURRENT APPLICATION NUMBER: US/11/186,284  CURRENT FILING DATE: 2005-07-21  PRIOR APPLICATION NUMBER: US 60/339,971  PRIOR APPLICATION NUMBER: US 60/339,971  PRIOR APPLICATION NUMBER: US 60/339,971  PRIOR APPLICATION NUMBER: US 60/331,978  PRIOR APPLICATION NUMBER: US 60/361,978  PRIOR APPLICATION NUMBER: US 60/361,978  PRIOR FILING DATE: 2002-03-05  PRIOR FILING DATE: 2002-05-20  NUMBER OF SEQ ID NOS: 228  SOFTWARE: FASTSEQ for Windows Version 4.0	ALIGNMENTS	348 23 1.7 170189 1 349 23 1.7 170285 1 350 23 1.7 172543 1 351 23 1.7 193789 1	344 23 1.7 150466 1 345 23 1.7 157224 1 346 23 1.7 164810 1 347 23 1.7 168656 1	341 23 1.7 34875 8 342 23 1.7 63693 8 343 23 1.7 139054 1	23 1.7 7006 8 23 1.7 11564 1 23 1.7 12277 8	335 23 1.7 5614 1 336 23 1.7 5727 1 337 23 1.7 5727 1	333 23 1.7 5011 7 334 23 1.7 5011 1	331 23 1.7 4677 8 332 23 1.7 4982 8	328 23 1.7 4314 7 329 23 1.7 4457 1 330 23 1.7 4642 1	326 23 1.7 4275 1 327 23 1.7 4290 1	324 23 1.7 3337 1 325 23 1.7 3958 1	322 23 1.7 3167 6 323 23 1.7 3293 8	319 23 1.7 3108 8 320 23 1.7 3147 8 321 23 1 7 3158 9	317 23 1.7 3073 1 318 23 1.7 3081 8	314 23 1.7 2805 1 315 23 1.7 2954 1 316 23 1.7 3050 1	313 23 1.7 2690 9 US-11-072-512-6
RESULT 1  US-11-186-284-208  US-11-186-284-208  Jequence 208, Application US/11186284  Publication No. US20050266493A1  Jeguran US20050266493A1  Jeguran US20050266493A1  Jeguran US20050266493A1  Jeguran US20050266493A1  Jeguran US20050266493A1  Jeguran Millennium Pharmaceuticals, Inc.  APPLICANT: Millennium Pharmaceuticals, Inc.  APPLICANT: Guillenette, Tracy L.  APPLICANT: Guillenette, Tracy L.  APPLICANT: Kamatkar, Shubhangi  APPLICANT: Monahan, John B.  APPLICANT: Honahan, John B.  APPLICANT: Burgart, Lawrence J.  APPLICANT: Burgart, Lawrence J.  APPLICANT: Burgart, Lawrence J.  APPLICANT: Burgart, Lawrence J.  APPLICANT: MONAHAN, John B.  Jerich OF INVENTION: METHODS FOR IDENTIFICATION, ANS  TITLE OF INVENTION: HERAPY OF COLON CANCER  FILLR REFERENCE: MEMO1-029P2RNM  CURRENT APPLICATION NUMBER: US/11/186,284  CURRENT APPLICATION NUMBER: US 60/339,971  PRIOR APPLICATION NUMBER: US 60/339,971  PRIOR APPLICATION NUMBER: US 60/361,978  PRIOR APPLICATION NUMBER: US 60/361,978  PRIOR APPLICATION NUMBER: US 60/361,978  PRIOR FILING DATE: 2002-03-05  PRIOR FILING DATE: 2002-05-20  NUMBER OF SEQ ID NOS: 228  PRIOR FILING DATE: 2002-05-20  NUMBER OF SEQ ID NOS: 228  SOFTWARE: FASTSEQ for Windows Version 4.0	ALIGNMENTS	348 23 1.7 170189 349 23 1.7 170285 350 23 1.7 172543 351 23 1.7 193789	344 23 1.7 150466 1 345 23 1.7 157224 1 346 23 1.7 164810 1 347 23 1.7 168656 1	341 23 1.7 34875 8 342 23 1.7 63693 8 343 23 1.7 139054 1	23 1.7 7006 8 23 1.7 11564 1 23 1.7 12277 8	335 23 1.7 5614 1 336 23 1.7 5727 1 337 23 1.7 5727 1	333 23 1.7 5011 7 334 23 1.7 5011 1	331 23 1.7 4677 8 332 23 1.7 4982 8	328 23 1.7 4314 7 329 23 1.7 4457 1 330 23 1.7 4642 1	326 23 1.7 4275 1 327 23 1.7 4290 1	324 23 1.7 3337 1 325 23 1.7 3958 1	322 23 1.7 3167 6 323 23 1.7 3293 8	319 23 1.7 3108 8 320 23 1.7 3147 8 321 23 1 7 3158 9	317 23 1.7 3073 1 318 23 1.7 3081 8	314 23 1.7 2805 1 315 23 1.7 2954 1 316 23 1.7 3050 1	313 23 1.7 2690 9 US-11-072-512-6
SULT 1 -11-186-284-208 -11-186-284-208 Sequence 208, Application US/11186284 Sequence 208, Application US/11186284 Sequence 208, Application US/11186284 Sequence 208, Application US/11186284 Sequence 208, Applicantim Pharmaceuticals, Inc. APPLICANT: Millemette, Tracy L. APPLICANT: Guillemette, Tracy L. APPLICANT: Kamatkar, Shubhangi APPLICANT: Monahan, John E. APPLICANT: Monahan, John E. APPLICANT: Monahan, John E. APPLICANT: Morenton, Novel Genes, COMPOSITIONS, TITLE OF INVENTION: MOTHOUS FOR IDENTIFICATION TITLE OF INVENTION: METHODS FOR IDENTIFICATION, TITLE REFERENCE: MPMO1-029P2RNM CURRENT APPLICATION NUMBER: US/11/186,284 CURRENT FILING DATE: 2005-07-21 PRIOR APPLICATION NUMBER: US 60/339,971 PRIOR APPLICATION NUMBER: US 60/339,971 PRIOR APPLICATION NUMBER: US 60/339,971 PRIOR APPLICATION NUMBER: US 60/361,978 PRIOR APPLICATION NUMBER: US 60/361,978 PRIOR FILING DATE: 2002-03-05 PRIOR FILING DATE: 2002-05-20 NUMBER: US 60/381,988 PRIOR FILING DATE: 2002-05-20	ALIGNMENTS	348 23 1.7 170189 12 US-11-112-908-50 349 23 1.7 170285 12 US-11-112-908-58 350 23 1.7 172543 12 US-11-121-086-6 351 23 1.7 193789 12 US-11-112-908-55	344 23 1.7 150406 12 US-11-112-908-51 345 23 1.7 157224 12 US-11-112-908-51 346 23 1.7 164810 12 US-11-121-086-4 347 23 1.7 168656 12 US-11-112-908-59	341 23 1.7 34875 8 US-10-775-169-316 342 23 1.7 63693 8 US-10-995-561-13269 343 23 1.7 139054 12 US-11-121-086-96	23 1.7 7006 8 US-10-821-234-218 23 1.7 11564 12 US-11-000-688-860 23 1.7 12277 8 US-10-477-507A-3	335 23 1.7 564.3 10 5-11-156-527-3578 336 23 1.7 564.4 12 US-11-136-527-3578 337 23 1.7 5727 12 US-11-136-527-599	33 23 1.7 5011 7 US-10-826-585-35 334 23 1.7 5011 12 US-11-045-578-3 356 33 1.7 5013 12 US-11-075-578-1	331 23 1.7 4677 8 US-10-821-234-114 332 23 1.7 4982 8 US-10-276-233A-17	328 23 1.7 4514 / US-10-826-595-2 329 23 1.7 4457 12 US-11-136-527-2981 330 23 1.7 4642 12 US-11-136-527-1815	326 23 1.7 4275 12 US-11-136-527-2433 327 23 1.7 4290 12 US-11-136-527-3034	324 23 1.7 3337 12 US-11-080-991-81 325 23 1.7 3958 12 US-11-169-041-94	322 23 1.7 3167 6 US-09-925-065A-21764 323 23 1.7 3293 B US-10-770-726-43	319 23 1.7 3108 8 US-10-4/7-50/AF-1 320 23 1.7 3147 8 US-10-947-249-51 321 23 1 7 3158 9 US-11-031-206-187	317 23 1.7 3073 12 US-11-113-424-11 318 23 1.7 3081 8 US-10-514-863-1	314 23 1.7 2805 1 315 23 1.7 2954 1 316 23 1.7 3050 1	313 23 1.7 2690 9 US-11-072-512-6
RESULT 1  US-11-186-284-208  US-11-186-284-208  Sequence 208, Application US/11186284  Publication No. US20050266493A1  GENERAL INFORMATION:  APPLICANT: Millennium Pharmaceuticals, Inc.  APPLICANT: Millennium Pharmaceuticals, Inc.  APPLICANT: Millennium Pharmaceuticals, Inc.  APPLICANT: Millennium Pharmaceuticals, Inc.  APPLICANT: Millenderte, Tracy L.  APPLICANT: Kamatkar, Shubhangi  APPLICANT: Monahan, John B.  TITLE OF INVENTION: METHODS COMPOSITIONS, KITS, AND TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, TILLE APPLICATION NUMBER: US/11/186,284  CURRENT APPLICATION NUMBER: US/11/186,284  CURRENT APPLICATION NUMBER: US 60/339,971  PRIOR APPLICATION NUMBER: US 60/339,971  PRIOR APPLICATION NUMBER: US 60/339,971  PRIOR APPLICATION NUMBER: US 60/331,978  PRIOR APPLICATION NUMBER: US 60/381,988  PRIOR FILING DATE: 2002-03-05  PRIOR FILING DATE: 2002-05-20  NUMBER OF SEQ ID NOS: 228  SOFTWARE: FastSEQ for Windows Version 4.0	ALIGNMENTS	348 23 1.7 170189 12 US-11-112-908-50 349 23 1.7 170285 12 US-11-112-908-58 350 23 1.7 172543 12 US-11-121-086-6 351 23 1.7 193789 12 US-11-112-908-55	344 23 1.7 150406 12 US-11-112-908-51 345 23 1.7 157224 12 US-11-112-908-51 346 23 1.7 164810 12 US-11-121-086-4 347 23 1.7 168656 12 US-11-112-908-59	341 23 1.7 34875 8 US-10-775-169-316 342 23 1.7 63693 8 US-10-995-561-13269 343 23 1.7 139054 12 US-11-121-086-96	23 1.7 7006 8 US-10-821-234-218 23 1.7 11564 12 US-11-000-688-860 23 1.7 12277 8 US-10-477-507A-3	335 23 1.7 564.3 10 5-11-156-527-3578 336 23 1.7 564.4 12 US-11-136-527-3578 337 23 1.7 5727 12 US-11-136-527-599	33 23 1.7 5011 7 US-10-826-585-35 334 23 1.7 5011 12 US-11-045-578-3 356 33 1.7 5013 12 US-11-075-578-1	331 23 1.7 4677 8 US-10-821-234-114 332 23 1.7 4982 8 US-10-276-233A-17	328 23 1.7 4514 / US-10-826-595-2 329 23 1.7 4457 12 US-11-136-527-2981 330 23 1.7 4642 12 US-11-136-527-1815	326 23 1.7 4275 12 US-11-136-527-2433 327 23 1.7 4290 12 US-11-136-527-3034	324 23 1.7 3337 12 US-11-080-991-81 325 23 1.7 3958 12 US-11-169-041-94	322 23 1.7 3167 6 US-09-925-065A-21764 323 23 1.7 3293 B US-10-770-726-43	319 23 1.7 3108 8 US-10-4/7-50/AF-1 320 23 1.7 3147 8 US-10-947-249-51 321 23 1 7 3158 9 US-11-031-206-187	317 23 1.7 3073 12 US-11-113-424-11 318 23 1.7 3081 8 US-10-514-863-1	314 23 1.7 2805 12 US-11-024-959-98 315 23 1.7 2954 12 US-11-241-347-2 316 23 1.7 3050 12 US-11-136-527-3575	313 23 1.7 2690 9 US-11-072-512-608 (
SMENT,	ALIGNMENTS	348 23 1.7 170189 12 US-11-112-908-50 349 23 1.7 170285 12 US-11-112-908-58 350 23 1.7 172543 12 US-11-121-086-6 351 23 1.7 193789 12 US-11-112-908-55	344 23 1.7 150406 12 US-11-112-908-51 345 23 1.7 157224 12 US-11-112-908-51 346 23 1.7 164810 12 US-11-121-086-4 347 23 1.7 168656 12 US-11-112-908-59	341 23 1.7 34875 8 US-10-775-169-316 342 23 1.7 63693 8 US-10-995-561-13269 343 23 1.7 139054 12 US-11-121-086-96	23 1.7 7006 8 US-10-821-234-218 23 1.7 11564 12 US-11-000-688-860 23 1.7 12277 8 US-10-477-507A-3	335 23 1.7 564.3 10 5-11-156-527-3578 336 23 1.7 564.4 12 US-11-136-527-3578 337 23 1.7 5727 12 US-11-136-527-599	33 23 1.7 5011 7 US-10-826-585-35 334 23 1.7 5011 12 US-11-045-578-3 356 33 1.7 5013 12 US-11-075-578-1	331 23 1.7 4677 8 US-10-821-234-114 332 23 1.7 4982 8 US-10-276-233A-17	328 23 1.7 4514 / US-10-826-595-2 329 23 1.7 4457 12 US-11-136-527-2981 330 23 1.7 4642 12 US-11-136-527-1815	326 23 1.7 4275 12 US-11-136-527-2433 327 23 1.7 4290 12 US-11-136-527-3034	324 23 1.7 3337 12 US-11-080-991-81 325 23 1.7 3958 12 US-11-169-041-94	322 23 1.7 3167 6 US-09-925-065A-21764 323 23 1.7 3293 B US-10-770-726-43	319 23 1.7 3108 8 US-10-4/7-50/AF-1 320 23 1.7 3147 8 US-10-947-249-51 321 23 1 7 3158 9 US-11-031-206-187	317 23 1.7 3073 12 US-11-113-424-11 318 23 1.7 3081 8 US-10-514-863-1	314 23 1.7 2805 12 US-11-024-959-98 315 23 1.7 2954 12 US-11-241-347-2 316 23 1.7 3050 12 US-11-136-527-3575	313 23 1.7 2690 9 US-11-072-512-608 (
DUND SMENT,	ALIGNMENTS	348 23 1.7 170189 12 US-11-112-908-50 349 23 1.7 170285 12 US-11-112-908-58 350 23 1.7 172543 12 US-11-121-086-6 351 23 1.7 193789 12 US-11-112-908-55	344 23 1.7 150406 12 US-11-112-908-51 345 23 1.7 157224 12 US-11-112-908-51 346 23 1.7 164810 12 US-11-121-086-4 347 23 1.7 168656 12 US-11-112-908-59	341 23 1.7 34875 8 US-10-775-169-316 342 23 1.7 63693 8 US-10-995-561-13269 343 23 1.7 139054 12 US-11-121-086-96	23 1.7 7006 8 US-10-821-234-218 23 1.7 11564 12 US-11-000-688-860 23 1.7 12277 8 US-10-477-507A-3	335 23 1.7 564.3 10 5-11-156-527-3578 336 23 1.7 564.4 12 US-11-136-527-3578 337 23 1.7 5727 12 US-11-136-527-599	33 23 1.7 5011 7 US-10-826-585-35 334 23 1.7 5011 12 US-11-045-578-3 356 33 1.7 5013 12 US-11-075-578-1	331 23 1.7 4677 8 US-10-821-234-114 332 23 1.7 4982 8 US-10-276-233A-17	328 23 1.7 4514 / US-10-826-595-2 329 23 1.7 4457 12 US-11-136-527-2981 330 23 1.7 4642 12 US-11-136-527-1815	326 23 1.7 4275 12 US-11-136-527-2433 327 23 1.7 4290 12 US-11-136-527-3034	324 23 1.7 3337 12 US-11-080-991-81 325 23 1.7 3958 12 US-11-169-041-94	322 23 1.7 3167 6 US-09-925-065A-21764 323 23 1.7 3293 B US-10-770-726-43	319 23 1.7 3108 8 US-10-4/7-50/AF-1 320 23 1.7 3147 8 US-10-947-249-51 321 23 1 7 3158 9 US-11-031-206-187	317 23 1.7 3073 12 US-11-113-424-11 318 23 1.7 3081 8 US-10-514-863-1	314 23 1.7 2805 12 US-11-024-959-98 Sequence 98 315 23 1.7 2954 12 III-241-347-2 Sequence 2. 315 23 1.7 3050 12 US-11-136-527-3575 Sequence 35	313 23 1.7 2690 9 US-11-072-512-608 Sequence 608
RESULT 1  US-11-186-284-208  Jequence 208, Application US/11186284  Publication No. US20050266493A1  Publication No. US20050266493A1  Jepulcant Information:  APPLICANT: Millenmium Pharmaceuticals, Inc.  APPLICANT: Monaham, John B.  JETILE OF INVENTION: MOYEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTIONS, MOYEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTIONS, MOYEL GENES, COMPOSITIONS, AND TITL	ALIGNMENTS	348 23 1.7 170189 1 349 23 1.7 170285 1 350 23 1.7 172543 1 351 23 1.7 193789 1	344 23 1.7 150406 12 US-11-112-908-51 345 23 1.7 157224 12 US-11-112-908-51 346 23 1.7 164810 12 US-11-121-086-4 347 23 1.7 168656 12 US-11-112-908-59	341 23 1.7 34875 8 US-10-775-169-316 342 23 1.7 63693 8 US-10-995-561-13269 343 23 1.7 139054 12 US-11-121-086-96	23 1.7 7006 8 US-10-821-234-218 23 1.7 11564 12 US-11-000-688-860 23 1.7 12277 8 US-10-477-507A-3	335 23 1.7 564.3 10 5-11-156-527-3578 336 23 1.7 564.4 12 US-11-136-527-3578 337 23 1.7 5727 12 US-11-136-527-599	33 23 1.7 5011 7 US-10-826-585-35 334 23 1.7 5011 12 US-11-045-578-3 356 33 1.7 5013 12 US-11-075-578-1	331 23 1.7 4677 8 US-10-821-234-114 332 23 1.7 4982 8 US-10-276-233A-17	328 23 1.7 4514 7 US-LU-826-353-2 329 23 1.7 4457 12 US-11-136-527-2981 330 23 1.7 4642 12 US-11-136-527-1815	326 23 1.7 4275 12 US-11-136-527-2433 327 23 1.7 4290 12 US-11-136-527-3034	324 23 1.7 3337 12 US-11-080-991-81 325 23 1.7 3958 12 US-11-169-041-94	322 23 1.7 3167 6 US-09-925-065A-21764 323 23 1.7 3293 B US-10-770-726-43	319 23 1.7 3108 8 US-10-4/7-50/AF-1 320 23 1.7 3147 8 US-10-947-249-51 321 23 1 7 3158 9 US-11-031-206-187	317 23 1.7 3073 12 US-11-113-424-11 318 23 1.7 3081 8 US-10-514-863-1	314 23 1.7 2805 12 US-11-024-599-98 Sequence 98, 315 23 1.7 2954 12 US-11-041-347-2. Sequence 2, 2 16 23 1.7 3050 12 US-11-136-527-3575 Sequence 3578	313 23 1.7 2690 9 US-11-072-512-608 Sequence 608

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LENGTH: 1141
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Best Local (
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NAME/KEY: CDS
LOCATION: (96)...(854)
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ORGANISM: Homo Sapiens
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                                                                                                         AGGGGACCCGGCTCCACACACACACACCCCCTAGAGAGCCCATCTGGAGCA 124:
                                                                                                                                    GCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGTGGGCCGCCTCCTTGCTGG
                                                                                                                                              AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 1001
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          CTGCGTAGGTGAAAAGGCAG 1321
                                            AAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGGCCGGGCTGGGG
                                                         AAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGGCCGGGCTGGGG
                                                                                        AGGGGACCCGGCTCCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCA
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RESULT 2 US-10-310-914A-7163/c US-10-310-914A-7163/ Application US/10310914A

US-10-310-914A-1106/c
US-10-310-914A-1106/c
; Sequence 1106, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

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APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detecta

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087,0200,CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PATENTIN VETSION 3.3

SEQ ID NO 6542

LENGTH: 97
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GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Schier, Kvuzat
TITLE OF INVENTION: Bioinformatically detectal
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 7163
LENGTH: 129
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US-10-310-914A-6542/c
US-10-310-914A-6542/c
; Sequence 6542, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; GENERAL INFORMATION.

                                                                                                                                                                                       ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-6542
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; ORGANISM: Human
US-10-310-914A-7163
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Best Local Similarity
Matches 128; Conserv
                                                                                                                             Matches
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Best Local
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                TCTCTAGGGTCCCCAGGGGGGCCGGGCTGGGGCTGCG 1306
                                                                             CGCGCCCCTAGAGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCC
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TCTCTAGGGTCCCCAGGGGGGCCGGGCTGGGGCTGCG
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RESULT 6
US-10-914A-7162/c
US-10-914A-7162/c
; Sequence 7162, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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; ORGANISM: Human
US-10-310-914A-1107
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; ORGANISM: Human
US-10-310-914A-1106
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FAPLICATION NUMBER: US/10/310,914A
CURRENT FILLING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
                                                        APPLICANT: Bentwich; Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
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APPLICANT: Shiler, Kvuzat
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5. US20060003322A1
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; Pred. No.
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                                                                                   group of novel regulatory genes and
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US-10-310-914A-399937/c

Sequence 399937, Application US/10310914A Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kvuzat TITLE OF INVENTION: Bioinfor TITLE OF INVENTION: uses

Kvuzat Bioinformatically detectable group of novel regulatory genes and RESULT 8

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; ORGANISM: Human
US-10-310-914A-7162
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                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-700
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                                                                                                                                                                      SOFTWARE: PatentIn Ver.
SEQ ID NO 700
LENGTH: 2332
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Best Local Similarity
                                                                                            Query Match
                                                              Matches
                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 4096
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION UNMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
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                                                                           Local Similarity 100.0%;
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1225 GAGGAGGAGGCGGCGGCGGCGGCGGCGG
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                               45 GAGGAGGAGGCGGCGGCGGCGGCGGCGG
                                                              31;
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INVENTION: Novel full length cDNA
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
                                                                                                                                                                                                                                                                                                                                                                                               SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAGAI, KEIICHI
IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                               NAGAHARI, KENJI
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YAMAMOTO, JUN-ICHI
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o. US20060029945A1
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                                                            Conservative
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GAI, KEIICHI
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                                                                             2.3%; Score 31; DB 9;
100.0%; Pred. No. 2e-05;
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Pred. No. 1.5e-
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                                                                Mismatches
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                                                                                             Length 2332;
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FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/L0/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID\_NOS: 1388402

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RESULT 9
US-11-112-944-14
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                                                                          SOPTWARE: PatentIn version 3.2
SEQ ID NO 144
LENGTH: 2947
TYPE DNA
ORGANISM: Rattus norvegicus
US-11-136-527-144
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US-11-136-527-144/c
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-944-14
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; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-399937
                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
     Best Loc
Matches
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Publication No. US20050244872A1
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Publication No. US20050287570A1
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CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,757
PRIOR FILING DATE: 2004-04-23
NUMBER OF SEQ ID NOS: 29
SOFTMARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Harris, Cole
TITLE OF INVENTION: Breast Cancer Gene Expression Biomarkers
FILE REFERENCE: 05-325-US
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Local Similarity 100.0%; F
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th 2.2%; Score 29; DB Similarity 100.0%; Pred. No. 0.0 (29; Conservative 0; Mismatches
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Pred. No. 0.00023;
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     DB 12; Length 2947;
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US-10-310-914A-100326

Sequence 100326, Application US/10310914A Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT:

Bentwich, Isaac Shiler, Kvuzat

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US-10-770-726-28/c
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US-10-770-726-28
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APPLICANT: Wyeth
APPLICANT: Hyeth
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AMIO1079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
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SEQ ID NO 28
LENGTH: 3131
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Publication No. US20050266459A1
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                                                                           Matches
                                                                                                               Query Match
                                                                                             Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                       APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICAT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILLING DATE: 2005-05-04
                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/567,570 PRIOR FILING DATE: 2004-05-04 NUMBER OF SEQ ID NOS: 107
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                                                                                                                                                                  LENGTH: 167891
TYPE: DNA
ORGANISM: Homo sapiens
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mes 29; Conservative
100185 GGCGGCGGCGGCGGCGGAGGCGC 100213
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                                     GGCGGCGGCGGCGGCGGAGGCGC 84
                                                                         Conservative
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k; Pred. No. 0.0
0; Mismatches
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Pred. No. 0.00018;
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0.0002;
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Best Local S
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Publication No. US20060024700A1
GENERAL INFORMATION:
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Publication No. US20060024700A1
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
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CURRENT APPLICATION NUMBER: US/10/310,914A
                                             CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
DBTOD BETTO PATTER TOTAL
                                                                                                                                APPLICANT: Hongjin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
                                                                                                                                                                               APPLICANT: Michele Cargill APPLICANT: Hongjin Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/568,846 PRIOR FILING DATE: 2004-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.3
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APPLICANT: Hongjin Huang
                                                                                                                   FILE REFERENCE: CL001519.ORD
                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Human
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CATION NUMBER: US 60/582,609
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100.0%; Pred. No. 0.0007;
ive 0; Mismatches (
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; Pred. No. 0.00074;
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US-11-124-367A-4192/c
                                                                                                                                                                                                                                                                                                                                 RESULT 17
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: Hongjin Huang
                                                                                                                                                                                                                                                                      Sequence 4204, Application US/11124367A Publication No. US20060024700A1
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR PILING DATE: 2004-06-25
PRIOR PILING DATE: 2004-08-09
PRIOR FILING DATE: 2004-08-09
PRIOR FILING DATE: 2004-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
                                                                                                                                                     TITLE OF INVENTION: Genetic Polymorphisms TITLE OF INVENTION: Fibrosis Methods of FILE REFERENCE: CL001519.ORD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: CL001519.ORD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
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%; Pred. No. 0.0
0; Mismatches
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Pred. No.
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RESULT 19
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; ORGANISM: Homo sapiens
US-11-124-367A-4257
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4204
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CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
PRIOR PRICING DATE: 2004-06-09
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
                                                                                                                                                                                                                                                                                                                     Sequence 4261, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: Hongjin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
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SEQ ID NO 4204
LENGTH: 201
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4257
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Best Local Similarity
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                                                             PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR PILING DATE: 2004-08-09
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
                                      SOFTWARE: FastSEQ for Windows Version 4.0
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b; Pred. No. 0.0
0; Mismatches
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; Pred. No.
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4274
                                                                               NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4274
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                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Use
FILE REFERENCE: CL001519.ORD
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/599,554 PRIOR FILING DATE: 2004-08-09
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Michele Cargill APPLICANT: Hongjin Huang
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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rative 0; Mismatches
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Pred. No. 0.0007;
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Pred. No. 0.0007;
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Length 201

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RESULT 23
US-11-124-367A-4329/c
US-11-124-367A-4329, Application US/11124367A
; Sequence 4329, Application US/11124367A
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US-11-124-367A-4325/c
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Best Local S
Matches 28
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LENGTH: 201
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Query Match
Best Local Similarity
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
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                                                                                                                                                                NUMBER OF SEQ ID NOS: 34460 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2004-08-09
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PRIOR FILING DATE: 2004-06-25
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/599,554
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                                                                               ORGANISM: Homo sapiens
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nes 28; Conservative (
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100.0%; Pred. No.
  2.1%;
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Score 28; DB 12; Length 201; Pred. No. 0.0007;
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0.0007;
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US-11-124-367A-4330/c
                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4342
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                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4342
LENGTH: 201
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Best Local
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CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
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ORGANISM: Homo sapiens
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                                                        Local Similarity
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                                   2.1%; Score 28; DB 12; ilarity 100.0%; Pred. No. 0.0007; Conservative 0; Mismatches 0
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; ORGANISM: Homo sapiens
US-11-124-367A-4396
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US-11-124-367A-4392/c
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APPLICANT: Michele Cargill
APPLICANT: Hongjin Huang
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                                                                                               Query Match
Best Local
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Publication No. US20060024700A1
                                                                              Matches
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Publication No. US20060024700A1
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PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSEQ for Windows Version 4.0
IEQ ID NO 4396
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CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
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PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hongjin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
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APPLICANT: Hongjin Huanq
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ORGANISM: Homo sapiens
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GAGGAGGCGGCGGCGGCGGCGG
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Pred. No.
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RESULT 28
US-11-124-367A-4397/c
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US-11-124-367A-4409/c
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; ORGANISM: Homo sapiens
US-11-124-367A-4397
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Best Local Similarity 100.0%;
Conservative
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                                                                                   Matches
                                                                                                                            Query Match
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CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
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CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR PILIOATION NUMBER: US 60/582,609
PRIOR PILING DATE: 2004-06-25
                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOPTWARE: FASTSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof FILE REFERENCE: CL001519.ORD
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Use
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
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ORGANISM: Homo sapiens
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                                                                                                         Score 28; DB 12; Pred. No. 0.0007
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Pred. No. 0.0007
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RESULT 30' US-11-124-367A-23494/c

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                                                              RESULT 32
US-11-124-367A-23496/c
                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-124-367A-23495
Sequence 23496, Application US/11124367A Publication No. US20060024700A1 GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
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LENGTH: 201
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CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR EILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Genetic Polymorphisms Associated with TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof FILE REFERENCE: CL001519.ORD CURRENT APPLICATION NUMBER: US/11/124,367A

CURRENT FILING DATE: 2005-05-09
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SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0.0007;
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CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR APPLICATION NUMBER: US 60/592,554
PRIOR FILING DATE: 2004-06-25
PRIOR PRIOR PRION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
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SEQ ID NO 23708
LENGTH: 201
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR ETITION NUMBER: US 60/599,554
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APPLICANT: Hongjin Ruang
TITLE OP INVENTION: Genetic Polymorphisms Associated with
TITLE OP INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2004-08-09 NUMBER OF SEQ ID NOS: 34460
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                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                    TYPE: DNA
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Local Similarity 100.0%; P
  142
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                                    51 GAGGAGGCGGCGGCGGCGGCGGCGG 78
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k; Pred. No. 0.0
0; Mismatches
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Pred. No.
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RESULT 34 US-11-024-959-254/c

Sequence 254, A Publication No.

Application US/11024959 o. US20060010516A1

GENERAL INFORMATION:
APPLICANT: FORSTER,
APPLICANT: CONNETT

FORSTER, RICHARD L. CONNETT, MARIE B. EMERSON, SARAH JANE

GRIGOR, MURRAY ROBERT

STEVEN TROY

COLLEEN M.

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US-11-124-367A-206/c
US-90-11-124-367A-206/c
Sequence 206, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:
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US-11-136-527-3064
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                                                                                                                                                                                                                                                                                               RESULT 36
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LENGTH: 2097
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TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044463-0360
CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 782
SOFTWARE: PatentIn version 3.3
                                                            APPLICANT: Michele Cargill
APPLICANT: Hongjin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCS: CL001519.ORD
CURRENT PPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
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PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
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                     PRIOR APPLICATION NUMBER: US 60/568,846 PRIOR FILING DATE: 2004-05-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Rattus norvegicus
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APPLICATION NUMBER; US 60/582,609
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100.0%; Pred. No.
1ve 0; Mismatches
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100.0%; Pred. No. 0.0
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; TYPE: DNA; ORGANISM: Homo Sapiens US-11-124-367A-207
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; ORGANISM: Homo Sapiens
US-11-124-367A-206
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APPLICANT: Michele Cargill
APPLICANT: Hongjin Huang
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PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: PRAESSEQ for Windows Version 4.0
SEQ ID NO 206
LENGTH: 12200
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Best Local
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR PILING DATE: 2004-06-25
                                                                                      APPLICANT: Michele Cargill
APPLICANT: Hongjin Huang
ITITE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Use
FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-05-07
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PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
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Pred. No. 0.00062;
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Pred. No. 0.00062;
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RESULT 39
US-11-124-367A-205/c
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 204
                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/11055035 Publication No. US20050256072A1 GENERAL INFORMATION:
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Best Local Similarity
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                                                       SEQ ID NO 2
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
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                                                                                                                                                     FILE REFERENCE: UMY-095
CURRENT APPLICATION NUMBER: US/11/055,035
CURRENT FILING DATE: 2005-02-09
                                                                                                                                                                                                              APPLICANT: ZAMORE, PHILLIP D.
APPLICANT: BRODERICK, JENNIPER
TITLE OF INVENTION: DUAL FUNCTIONAL OLIGONUCLEOTIDES FOR USE IN REPRESSING
TITLE OF INVENTION: MUTANT GENE EXPRESSION
                                                                                                                PRIOR APPLICATION NUMBER: 60/543,467 PRIOR FILING DATE: 2004-02-09
                                                                                                                                                                                                                                                                     APPLICANT: ARONIN, NEIL APPLICANT: ZAMORE, PHII
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PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
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APPLICANT: Hongjin Huang
                                                                           SOFTWARE: PatentIn Ver. 3.3
                                                                                               NUMBER OF SEQ ID NOS: 107
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ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
                                    ENGTH:
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; Pred. No. 0.00062;
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RESULT 43
US-10-310-914A-20511
US-10-310-914A-20511, Application US/10310914A
Publication No. US20060003322A1

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Query Match
Best Local Similarity
Watches 27; Conserv
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US-10-310-914A-4814
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                                                                                                                          ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-12973
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US-10-310-914A-12973
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; ORGANISM: Human
US-10-310-914A-4814
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SEQ ID NO 4814
LENGTH: 110
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Best Local
                                                                                                                                                                                                                                                                                                                                                        Sequence 12973, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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                                                                                                                                                                          SOFTWARE: PatentIn version 3.3
SEQ ID NO 12973
LENGTH: 110
                                                             Matches
                                                                                           Query Match
                                                                                                                                                                                                                                         APPLICANT: Shiler, Kvuzat, TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
                                                                                                                                                                                                                                                                                                                         APPLICANT: Bentwich, Isaac APPLICANT: Shiler, Kyuzat
                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 1388402
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                                                                              Similarity
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                              AGGAGGAGGCGGCGGCGGCGGCGG 75
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AGGAGGAGGCGCCGCCGCCGCCGC
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; Pred. No. 0.00062;
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                                                                            Score 27; DB 8; Pred. No. 0.002
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Pred. No. 0.0023;
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                                                                              .0023;
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; Sequence 373740, Application US/09925065A
; Publication No. US20040181048A1
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PRIOR FILLING DATE: 2000-10-24
PRIOR PELLOATION NUMBER: US 60/252,147
PRIOR FILLING DATE: 2000-11-20
PRIOR FILLING DATE: 2000-11-30
PRIOR FILLING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILLING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILLING DATE: 2001-05-09
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 20511
                    Sequence 540849, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

PILE REFERENCE: 108827.135
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 10827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows
EQ ID NO 373740
CURRENT APPLICATION NUMBER: US/09/925,065A
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; Pred. No. 0.0023;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-540850
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PELICATION NUMBER: US 60/252,147
PRIOR PELICATION NUMBER: US 60/250,092
PRIOR PELICATION NUMBER: US 60/261,766
PRIOR PELICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR PILING DATE: 2001-01-05-09
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
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US-09-925-065A-540850
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RESULT 47
US-09-925-065A-499554/c
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 540849
                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 540850
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                                                                                                                                                                                             Query Match
Best Local Similarity
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PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
DEIOR STITMG DATE: 2001-11-16
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PRIOR FILING DATE: 2000-10-24
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PRIOR APPLICATION NUMBER: US 60/289,846
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                                                                                                                                                                                                                                                                                                                             LENGTH: 583
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Local Similarity 100.0%;
hes 27; Conservative
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                                                                                                                                                                           0;
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Pred. No. 0.0022;
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Pred. No. 0.0022;
                                                                                                                                                                        Mismatches
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Sequence 499554, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

AITTLE OF INVENTION: Identification and Mapping of Single

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RESULT 48
US-11-136-527-2759
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                                                                                                      Sequence 2522, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
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Publication No. US20050287570A1
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Best Local
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Best Local Similarity
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TITLE OF INVENTION: Probe Arrays For Expression Profiling
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
NUMBER OF SECOLUTION OF THE PRIOR PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Publication No. US200 GENERAL INFORMATION:
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-09-925-065A-499554
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
                                      CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
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APPLICATION NUMBER: US 60/289,846
APPLICATION NUMBER: US 60/574,294
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Search completed: February 28, 2006, 11:27:00 Job time : 485 secs

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; ORGANISM: Bovine
US-10-750-185-34757
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SEQ ID NO 2522
LENGTH: 2074
TYPE: DNA
ORGANISM: Rattus norvegicus
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Best Local Similarity
                                                                                                                                                                                                  SEQ ID NO 34757
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NUMBER OF SEQ ID NOS: 362830
                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/437,482 PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MMI GENOMICS, INC. APPLICANT: DENISE, Sue K.
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMIl100-2
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1117 GGAGGCGGCGGCGGCGGCGGCGG 1142
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score greater than or equal to the score of the result being printed,
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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## ALIGNMENTS

AX392417 Sequence 1 from Patent WO0216416.  AX392417.1 GI:19700732 Homo sapiens (human) Homo sapiens (buman) Homo sapiens (buman) Homo sapiens (chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Hominidae; Homo.  1 Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and Turi, T.G. Diagnosis and treatment of cardiovascular conditions Patent: WO 0216416-A 1 28-FEB-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); PFIZER INC. (US) Location/Qualifiers Locat	Query Match Best Local Si Matches 1321;	ORIGIN	CDS	TITLE JOURNAL FEATURES	SOURCE SOURCE ORGANISM REFERENCE AUTHORS	RESULT 1 AX392417 LOCUS DEFINITION ACCESSION VERSION
	100.0%; Score 1321; DB 6; Length 1321; Similarity 100.0%; Pred. No. 5.3e-142; 1; Conservative 0; Mismatches 0; Indels 0; Gaps	/codon_start=1 /protein_id="cAD29005.1" /protein_id="cAD29005.1" /db_xref="di:19700733" /db_xref="di:19700733" /translation="MHRLMGVNSTAAAAAGQENVSCTCNCKRSLFQSMEITELEFVQ /translation="MHRLMGVNSTAAAAAGQENVSCTCNCKRSLFQSMEITELEFVQ /translation="MHRLMVPHAAAAAGRERHRFQBTXLGGERCLMPSESTVSGIITEVVMMYMVVITCLLSHYKLSAARSFISHESQGRREDALSSEGCLMPSESTVSGIEEPP GIFERQVYAAPPRFUDRLAVPFFAAREKFHRFQFTYFQHQHIDLPFTISLSDGEEPP YQGPCTLQLRDFBQQLELMRESVRAFENRTIFDSDLMDSARLGGPCPESSNSGISAT YGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIW KEKDKQKGHPL"	~ ~ ~ ~ ~ .		(human etazoa; theria; omo.	1321 bp DNA linear 1 from Patent WO0216416.

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7	961 GCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGG 1020
VQ dq	901 CCCCTGCACCTTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGT 960
ν γς d	841 GATCGACCTGCCACCCACCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGG 900
P VQ	781 CTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGA 840
D Qy	721 AATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCG
Que Bee	661 AGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGG 720
ORIG	601 CCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGCGGAGGAGAGA 660
FEATU	541 GATCATCATCATCGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGCCTGCTGAG 600
REFEI AUT TIJ	481 GTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCA 540
ORO	421 CTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGGCGGGCAGCCCAATGTCTCCCTGCAC 480
ACCES VERSI KEYWO SOURO	361 CCCCGGCCCCCGAGCCCCCCGCGCGCCGCGCGCGCGCCGC
RESUI CS13 LOCUS	301 CTCCCCGCCGCGCGCCTCCTGCATGCGGGGCCCAGCTCCGGGCGCCGGAGCCCC 360
da	241 TGAGCCCCGCGGCGCCCCCGGGAACTTGGCGGCGACCCGGAGCCCGGGGCGAGCCGGGGCGCGC 300
od da	181 ACGCCCCCGGGGCTGCCGAGGGGAGGCCGGGGGGGCGCAGCGGAGCGCGGTCCCGCGCAC 240
OV DD .	121 GGCGGCAGCGCGCGCCCGCTGCCAGCCCATTTTCCGGACGCCACCCGCGGGCACTGCCG 180
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Patent: WO 2005064009-A 82 14-JUL-2005;
Aros Applied Biotechnology APS (DK)
Location/Qualifiers
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Sequence 82 from Patent
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CS130796.1 GI:71792866
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/organism="Homo sapiens" /mol type="unassigned DNA" /db xref="taxon:9606" 1. .4839 /note="NM\_020182" DNA" Length

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TGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCA TGGTGGTGGTGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCA 540 632 692

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1 GAAAGCTAGCGGCAGAGGCTCAGCCCCGGGGGGCAGCCGCGCGCG	Query Match Query Match 93.0%; Score 1229; DB 6; Length 4839; Best Local Similarity 100.0%; Pred. No. 1.2e-131; Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	j D	Beckmann, Xinzhong, Human nuc	ria; Euarchontoglires; Primates; Catarrh	Homo sapiens (human) Homo sapiens	CQ896247 ON Sequence 71 from CQ896247 N CQ896247 1 GI.ES	1201 ODDE LODDSE LOCAL DES LOS LOS LOS LOS LOS LOS LOS LOS LOS LO	1293 GGGCTGGGGCTGCGTAGGTGAAAAGG	1233 TCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGG	1173 CCTTGCTGGAGGGACCCGGCTCCACCACACACACTCGCGCCCCTAGAGAGCGCAGCCA 1	1113 AGGTCATCGGCCA	P	993 GTGACCTGATGGATAGTGCCAGGCTGGGGGGCCCCTGCCCCCCAGCAGTAACTCGGGCA 1	933 AGCAGCTGGAACTGGAACCGGGAGTCGGTGGCGCACCCCCAAACAGAACCATCTTCGACA	Qy 873 ACGGGGAGGAGCCCCACCCTACCAGGGCCCCTGCACCTTCCAGCTTCGGGACCCCGAGC 932
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                                                                                                      TGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGA
                                                                                                                                              CCGCCGGGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCA
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                         GCCGGCACAGCCAGGGGGGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGC
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                                                                   TGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCA
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166 from Patent WO2004113571.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence
CQ981430
                                                                                                                                                  Rosenthal, A., Hermann, K., Heiden, E., Pilarsky, Staub, E., Roepcke, S., Mennerich, D., Kinnemann, Human nucleic acid sequences from lung tumous patent: EP 1498424-A 285 19-JAN-2005; Heinemann, Bernd (DE); Hermann, Klaus (DE); Heinemann, Bernd (DE); Hermann, Klaus (DE);
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                              CQ981430.1
                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                          Rosenthal, Andre (DE)
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                                                          /organism="Homo sapiens"
/mol_type="unassigned DN/
/db_xref="taxon:9606"
                                                                                                        Location/Qualifiers
1. .4839
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93.0%;
100.0%;
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 Score 1229; DB 6;
Pred. No. 1.2e-131;
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Submitted (14-SEP-2000) Centre for Molecular Biotechnology,
Queensland University of Technology, 2 George St, Brisbane,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                     GGAAAGCTAGCGGCAGAGGCTCAGCCCCGGCGGCGGCAGCGCCCCGCCGCCGCCCCGCTGCCCATT
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/db_xref="taxon:9606"
/chromosome="20"
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Patent: WO 03048202-A 159 12-JUN-2003;
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TGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGA
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VQGPCTLQLRDFEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCFPSSNSGISATC
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(DE); Pilarsky, (DE); Lichtner,

Christian Rosemarie

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REFERENCE
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Sequence 2 from Patent
CQ894692
CQ894692.1 GI:55467441
Rosenthal, A.D., Pilarsky, C., Dahl, E., Spec
Lichtner, R., Staub, E., Rospcke, S. and Li, J
Human nucleic acid sequences expressed in
Patent: EP 1471075-A 2 27-OCT-2004;
                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                             Homo sapiens
                                                           Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                GGGTCCTTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAGGGGACCCGG
                                                                                                                                            ACCGCCGGCCCATGGAGGGCCCCCCCCCCCACGGCGAGGTCATCGGCCACTACCCG
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                                                CTCCACCACACACACACCGCGCCCCTAGAGAGGCGCAGCCATCTGGAGCAAAGAGAAGGAT
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1. .4519
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carrinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Wong, A.C., Shevchenko, Y.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, R.M., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
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Homo sapiens transmembrane, prostate androgen induced RNA,
(cDNA clone IMAGE:4559576), partial cds.
BC015918
      Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.geries: IRAL Plate: 29 Row: e Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                      Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquiet, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTB
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (15-OCT-2001) National Institutes of Health, Mammalian Submitted (16-OCT-2001) Cancer Genemics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC015918.1 GI:16198474
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Contact: MGC help desk
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
This clone was selected for ful passed the following selection
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                   information can be found http://image.llnl.gov
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                                                              GGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCC
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/note="BCAS2; Region: Breast carcinoma amplified sequence / (BCAS2). This family consists of several eukaryotic sequences of unknown function. The mammalian members of this family are annotated as breast carcinoma amplified sequence 2 (BCAS2) proteins. BCAS2 is a putative spliceosome associated protein"
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/db_xref="MIM:606564"
/db_xref="MIM:606564"
/db_xref="MIM:606564"
/translation="NSTAAAAAGQPNVSCTCNCKRSLFQSMEITELEFVQIIIIVVM
MVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLMPSESTVSGNGIPEPQV
YAPRRPTDRLAVPFFAQRERFHRFQFTYFYLOHEIDLPFTISLSDGEEFPPYQGFCTL
QLRDDEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNSGISATCYGSGGRM
EGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWSKEKDKQK
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/product="TMEPAI protein"
/protein_id="AAH15918.2"
/db_xref="GI:45946553"
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db_xref="GeneID:56937"
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'clone_lib="NIH_MGC_14"
'lab_host="DH10B-R"_
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Sequence 3 from Patent WO0216416
AX392419
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 ATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGCCGCCGGGCAGCCCAATGTC
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ilarity 100.0%;
Conservative (
                                                                                                    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                            note="unnamed protein product"
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                        Score 861; DB 6;
Pred. No. 2.1e-89;
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JP 2002539773-A/3.
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  Hominidae; Homo.
1 (bases 1 to 969)
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                      Homo sapiens (human)
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Secreted proteins and nucleic acids encoding them
L Patent: JP 2002539773-A 3 26-NOV-2002;
MILLENNIUM PHARMACEUTICALS INC
OS Homo sapiens (human)
pJ 2002539773-A/3
PD 26-NOV-2002
PF 01-MAR-2000 JP 2000602247
PF 01-MAR-1999 US 60/122458
PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRI
PI FRASER
C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12
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THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER
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/mol_type="genomic DNA"
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Homo sapiens PMEPA1 protein (
AF224278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu,L.L., Shanmugam,N., Se Moul,J.W. and Srivastava,
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Moul,J.W. and Srivastava,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 1141)
               Similarity
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                                                                                                                                                                                                /note="type 1b transmembrane protein; expression is induced in response to the synthetic androgen, R1881; expression is abundant in, and restricted to, prostat glandular epithelial cells; similar to the predicted protein encoded by sequence deposited at GenBank Acce
                                                                 Number NP_004329"
                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
/mol_type="mRNA"
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             60.7%;
 Score 802.2; DB 8 Pred. No. 9.9e-83; 0; Mismatches 13
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                       Classification of cancer Patent: WO 2005064009-A 127 14-JUL-2005; Aros Applied Biotechnology APS (DK)
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Mammalia; Eutheria;
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812	1713	1713	1713	1713	693	1583	878	759	759	759	1069	806	1066	4531	1334	1085	1061	1140	1140	1140	969	969	969	4538	4527
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AAZ52964	AAA75168	AAA75166	AAA75167	AAA75152	ABK12143	ABS61424	ABK12142	ADO39827	ADH62277	ADF17545	AAI59654	ACC49537	AAI57868	AEB22833	ABZ36103	ADC37324	AAA47429	ADO39826	ADH62276	. AAD60105	AAA75165	AAA75163	AAA75164	AEB22832	ADV85880
Aaz52964 Human pro		CDNA		CDNA	Humai			Ado39827 Human PME	Human	Adil 17545 Human and	Aai59654 Human pol		Aai57868 Human poi	Aeb22833 Human col	Abz36103 Human sec	Adc37324 Nuclear I	Aaa47429 Sequence	Ado39826 Human PME	Adh62276 Human PME	Aad60105 Human and	Aaa75165 cDNA clon		CDNA	N	Adv85880 Human ARP

## ALIGNMENTS

RESULT 1 ABK12137

ABK12137 standard; cDNA; 1321 BP.

05-JUN-2002 ABK12137;

(first entry)

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cytostatic; cardiant; cerebroprotective; antiarteriosclerotic; cardiac cell; anti-apoptotic; vascular endothelial cell; cardiac hypertrophy; myocardial infarction; stroke; arterioscleheart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
Novel nucleic acid molecule encoding Mechanically Induced Vascular Receptor-1 polypeptide, useful for treating cardiovascular diseases
                                                                                                                                                                                                                                                                           22-AUG-2000; 2000US-0227159P
                                                                                                                                                                                                                                                                                                                       21-AUG-2001; 2001WO-US026089
                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2002.
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                                                                          WPI; 2002-280912/32
P-PSDB; AAU78231.
                                                                                                                                                                                                   (BGHM )
(PFIZ )
                                                                                                                                                     Lee RT,
                                                                                                                                                                                                   BRIGHAM & WOMENS HOSPITAL INC. PFIZER INC.
                                                                                                                                                     Landschulz KT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "MIVR-1"
/note= "This region is specifically claimed in claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                     Kennedy SP,
                                                                                                                                                       Thompson JF,
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ADB75588 ACC49536

ADL83313

Acc49536 Tumour-as Adl83313 Human and Abk92120 Prostate

Adb75588 Prostate

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid molecule encoding a CC Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having CC cardiac cell anti-apoptotic activity and fragments of it provided they CC are not identical to Genbank sequences A1761441.1, A1594390, NM 004338 CC and A0177461. Also included are expression vectors, host cells, the MIVR-CC in polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting CC a molecule having cardiac cell anti-apoptotic activity with a candidate CC eigent, where the molecule is a nucleic acid molecule comprising MIVR-1, CC IEX-1, VDUP-1, BTG-2 and TIS-11d or its expression product, determining CC if the anti-apoptotic activity is modulated and thereby identifying a CC of the invention are useful for treating, diagnosing and monitoring CC progression of such diseases and disorders as characterised by increased CC apoptotic cell-death of vascular endothelial cells e.g. cardiac CC hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart CC failure. The present sequence encodes human MIVR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 1321; Conserv
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AGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGG
                                                 CCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGCCAGGGGGCGGAGGAGAGA
                                                                                                                 GATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGCCTGAG
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Pred. No. 3e-198;
0; Mismatches 0;
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 27-DEC-2003;
24-JAN-2004;
07-APR-2004;
26-NOV-2004;
                                                                                                                                      cancer; genetic marker; lymphoma; cytostatic; hematological disease;
immune disorder; neoplasm; colon tumor; gastrointestinal disease;
adenocarcinoma; carcinoma; screening; diagnostic; prognostic;
pharmaceutical; ds; gene.
                                                                          14-JUL-2005.
                                                                                                                                                                                            Human colon
                                                                                                                                                                                                                                                          AEB22787 standard;
                                                     23-DEC-2004;
                                                                                               WO2005064009-A1.
                                                                                                                                                                                                                 22-SEP-2005
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; 2003DK-00001940.
; 2004DK-0000096.
; 2004DK-00000586.
; 2004DK-00001843.
                                                                                                                                                                                            cancer-associated gene SEQ ID
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                                                     2004WO-DK000914
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Matches 1302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising at least one marker capable of determining the microsatellite status in a sample and at least one marker in a sample determining the prognostic marker, where the microsatellite status and the prognostic marker is determined simultaneously or sequentially. The method above is useful for producing an assay for classifying cancer in animal tissue. The peptide, gene, or probe is useful for preparing a pharmaceutical composition for the treatment of a cancer in animal tissue. The method is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4930 BP; 1133 A; 1331 C; 1324 G; 1142 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microsatellite status or the hereditary or sporadic nature of the cancer; (b) determining the presence and/or amount of the gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hereditary or sporadic nature of the cancer is determined by a method comprising: (a) obtaining a sample from the individual having contracted cancer, the sample comprising gene expression products, the presence and/or amount of which forms a pattern that is indicative of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of classifying the cancer in an individual having contracted cancer, which comprises determining the microsatellite status of the tumor. The microsatellite status or the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; SEQ ID NO 82; 338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Classifying the cancer in an individual having contracted cancer comprises determining the microsatellite status of the tumor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for classifying the cancer in an individual having contracted cancer, i.e. colon cancer, e.g. an adenocarcinoma, a carcinoma, a teratoma, a sarcoma, and/or a lymphoma. The present sequence represence colon cancer-associated gene used in the method of the invention.
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                                                                                                                                                                                                                                                                              GGCGCTCGGCTGGGGAAAGCTAGCGGCAGAGGCTCAGCCCCGGCGGCAGCGCGCCCCCG
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  GGGGAGGCCGGGGGGGGCGCAGCGGAGCGCGCGCACTGAGCCCCGCGGCGCCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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mammals. The invention also relates to nucleic acid and polypeptide CC sequences at least 80% identical to the TAT nucleic acids and comparising a TAT nucleic cody, an antibody specific for a TAT polypeptide; a peptide or organic complecule which binds to a TAT polypeptide; fusion proteins comprising a TAT nucleic cody, an antibody specific for a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or cody, and the cancer in mammals. TAT polypeptides, nucleic acids, concert in mammals. TAT polypeptides, nucleic acids, concert in mammals. TAT polypeptides nucleic acids, concert, antagonists, binding molecules and compositions are useful concerts. The concerts are concerts of the cancer, colorectal cancer, lung cancer, ovarian cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central cancer, pancreatic cancer, cervical cancer, cancers of the central cancers as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence corporesents a TAT nucleic acid of the invention
                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rumour-associated antigenic target; TAT; human; overexpression; c tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tumor-associated antigenic target polypeptides and nucleic useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in
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19-OCT-2001; 2001US-0339227P.
07-NOV-2001; 2001US-0336827P.
20-NOV-2001; 2001US-0331906P.
20-NOV-2001; 2002US-034944P.
03-APR-2002; 2002US-0369724P.
19-AUG-2002; 2002US-0404809P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frantz G,
Williams
                                                                                                                                                                                                                              ACC49493 to ACC49552 encode the human tumour-associated antigenic target (TAT) proteins given in ABP97175 to ABP97234. The present invention describes an isolated antibody that binds to a polypeptide having at least 80 % sequence identity to any of the 60 150-800 residue amino acid sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking its associated signal peptide, encoded by any of the 60 2000-3000 base pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have cytostatic activity. The antibody can be used for treating or diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal cell carcinomas, or thyroid cancer
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M, Wu TD,
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100.0%; Pred. No. 7.2e-184;
ative 0; Mismatches 0;
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                                                                                                                                                                                     autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA chairment that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene expression of at least 60% of the genes correlates with that of the gene expression of a the least 60% of the genes for targeting in the treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis; in a mammal other than a mouse; diagnosis of rheumatoid arthritis; diagnosis or cher than a mouse; diagnosis of rheumatoid arthritis; diagnosis or array or gene chip, specific for rheumatoid arthritis; diagnosis or carray or gene chip, specific for rheumatoid arthritis; diagnosis or carray or gene chip, specific for rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collagentinduced arthritis; and reducing the symptoms associated with collagentinduced arthritis. The compositions of the invention have the following activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic, antiput, and compositions of the present invention are useful for the analysis of the present invention are useful for the analysis and treating autoimmune disease or arthritides, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disease; arthritide; gene expression analysis; rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic; antiarthritic; osteopathic; antigout; antiinflammatory; dermatological; immunomodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgia; osteopathritis; gout; juvenile rheumatoid arthritis;
                              rheumatoid arthritis, lupus, ankylosing spondylltis, fibrositis, ifibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an immune disease caused by an infectious agent. This polynucleotide represents a DNA sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritides. Note: This sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and the state of th
                                                                                                                                                                    diagnosing rheumatoid
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The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis; diagnosis or array or gene chip, specific for rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; screening the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disease; arthritide; gene expression analysis; rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatiantiarthritic; osteopathic; antigout; antiinflammatory; dermatological; immunomodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
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                                                                                                                                                                                                                                                       Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia
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induced arthritis. The compositions of the invention have the following
activities: immunosuppressive, antirheumatic, antiarthritic, osteopathi
antigout, antiinflammatory, dermatological, and immunomodulatory. The
methods and compositions of the present invention are useful for
diagnosing and treating autoimmune disease or arthritides, such as
rheumatorid arthritis, lpus, ankylosing spondylltis, fibrositis,
fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and
immune disease caused by an infectious agent. This polynucleotide
represents a DNA sequence relating to the genes used in the analysis an
treatment of autoimmune diseases or arthritides. Note: This sequence is
not shown in the specification. It has been supplied in an electronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; adipocyte specific; ds; adipose tissue; anti-obesity; high mobility group I-C protein; HMGI-C; obesity; leptin; ob; adipogenesis; hypertension; cardiovascular disease; anorectic; antidiabetic; hypotensive.
This invention relates to a novel method for identifying genes that
                                                Claim 11; SEQ ID NO 180; 91pp; English.
                                                                                            Identifying adipocyte specific genes, useful for treating obesity or diabetes, and for identifying drug targets, by differential gene expression analysis between adipose tissue or stromal vascular tissumice of different genotypes.
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HERMANN K.
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useful for diagnosis, treatment and ä screening for specific binding

German

This invention describes novel cytostatic polynucleotide and polypeptide cor the risk of developing prostatic cancer. Diagnosis is based on the risk of developing prostatic cancer. Diagnosis is based on compositatic cancer cancer. Diagnosis is based on the risk of developing prostatic cancer. Diagnosis is based on compositatic cancer. Diagnosis is based on the prostatic cancer can be called the cancer of the sequences in prostatic cancer involves a binding assay, any compounds that bind are composited the cancer of the sequences or detection of a publicated minimum level of the reporter indicates the presence of the unour cells. Inhibitors can be chosen from antisense oligonucleotides, compounds that bind are composited the presence of the prostatic profession of a predetermined minimum level of the reporter indicates the presence of the unour cells. Inhibitors can be chosen from antisense oligonucleotides, and the composite the polypeptide, preferably 300, that binds to the polypeptide; an the polypeptide profession and the polypeptide, and the polypeptide, and or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polymucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that the prostatic cancer patients, or subjects at risk, were incubated from prostatic cancer patients, or subjects at risk, were incubated from prostatic cancer patients. The monoclonal antibodies; and then diaminobenzidine as colour former (brown). The graphes were counterstained with hemalum (blue). Malignant cells stained cancer samples of cancercinoma, membrane and cytoplasmic staining was very strong, and colour invention.

Sequence 4839 BP; 1103 A; 1313 C; 1290 <u>ი</u> 1133 T; 0 u; o Other;

Matches 1229; Query Match Best Local Similarity Conservative 93.0%; Score 1229; DB 13; pred. No. 7.2e-184; 0 ; Mismatches 0 Indels Length 4839; 0 Gaps

á 닭 á 뭐 S 밁 S 당 8 밁 Ś 밁 S 吊 S 513 361 453 301 393 241 333 181 273 121 213 421 153 13 93 Н GGGCGCAGCGGAGCGCGGTCCCGCGCACTGAGCCCCGGGGGCGCCCCCGGGAACTTGGCGGC TTCCGGACGCCACCCGCGGGACTGCCGACGCCCCCGGGGCTGCCGAGGGGAGGCCGGGG TGGAGATCACGGAGCTGGAGTTTTGTTCAGATCATCATCATCGTGGTGATGATGATGGTGA GACCCGAGCCCGGCGAGCCCGCGCGCGCCCCCCCCGCGCGCCTCCTGCATGCGGGGC GGGCGCAGCGGAGCGCGCTCCCGCGCACTGAGCCCCGCGGCGCCCCCGGGAACTTGGCGGC GEANAGCTAGCGGCAGAGGCTCAGCCCCGGCGGCAGCGCGCGCCCCGCTGCCAGCCCATT CCGCCGGGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCA GCCGCGCCGCCGCCGTCCATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCG CCCAGCTCCGGGCGGCCGGAGCCCCCCCCCGGGCCCCCGAGCCCCCGGGGCCCCG 480 420 512 360 452 300 392 240 332 180 272 120 212 60

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GACCCGAGCCCGGCGAGCCCGGGGGCGCGCCTCCCCGCGGGGGCGCTCCTGCATGCGGGGC 332

GGGCGCAGCGGAGCGCGCGCCCCCGCGCGCCCCCGCGGGGAACTTTGGCGGC TTCCGGACGCCACCCGCGGCACTGCCGACGCCCCCGGGGCTGCCGAGGGGAGGCCGGGG

GGGCGCAGCGGAGCGCGCTCCCGCGCACTGAGCCCCCGCGCGCCCCCGGGAACTTGGCGGC

180

120 272

212 60 Matches 1229; Query Match

93

153 61

Local

Similarity

93.0%; Score 1229; DB 13; 100.0%; Pred. No. 7.2e-184;

Conservative

0

Mismatches

Indels Length

Gaps

0

Sequence

4839 BP; 1103 A; 1313 C; 1290 G; 1133 T;

0 U; 0 Other;

4839; <u>,</u>

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This invention describes novel cytostatic polynucleotide and polypeptide cor the risk of developing prostatic cancer. Diagnosing prostatic cancer determining over transcription or over expression of the sequences in corpostatic tissue. Screening for inhibitors of the sequences in corpostatic tissue. Screening for inhibitors of the sequences or detection corpostatic cancer corpostatic tissue. Screening for inhibitors of the sequences or detection corpostatic tissue. Screening for inhibitors of the sequences or detection corpostatic potionally after deconvolution of mixtures. Detection of a corpostatic potionally after deconvolution of mixtures. Detection of a corpostatic cancer inhibitors can be chosen from antisense oligonucleotides, corpostatic potions and the polypeptide; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an corpostatic polypeptide, preferably humanised or human; an anti-idiotype, non-human corpostatic preferably humanised or human; an anti-idiotype, non-human corpostatic properties, and the polypeptide; and the polypeptide, and the polypeptide; and the polypeptide, preferably humanised or human; the polypeptide; and corpostatic cancer by differential expression analysis, using DNA microarrays, corpostatic cancer by differential expression analysis, using DNA microarrays, corpostatic cancer patients, or subjects at risk, were incubated that the polypeptide properties and then diaminobenzidine as colour former (brown). The sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained conjugated horseradish the polypeptide sequences used in the method of the conjugation.
(DAHL/)
(ROSE/)
(HERM/)
(PILA/)
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14-MAY-2003; 2003DE-01022134.
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Schmitt A,
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ROSENTHAL A.
HERMANN K.
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Beckmann (
Staub E;
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3, Bruemmendorf T, Kinnemann H, Roe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded proteins,
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Roepcke S;
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                                                                                   TCTGGAGCAAAGAGAAGGATAAACAGAAAAGGACACCCTCTCTAGGGTCCCCCAGGGGGGGCC
                                                                                                                                                   CCTTGCTGGAGGGGACCCGGCTCCACCACACACACACACTCGCGCCCCCTAGAGAGCGCAGCCA
                                                                                                                                                                                                           AGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCT
                   GGGCTGGGGCTGCGTAGGTGAAAAGGCAG 1321
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                                                                                                                                                                                                                                                                                                                        This invention relates to a novel isolated nucleic acid associated with CC bronchial cancer comprising 489 defined sequences given in the CC specification. The invention may be useful for the production of CC compounds with a cycostatic activity through the inhibition of expression CC compounds with a cycostatic activity through the inhibition of expression CC concern for tumour-associated proteins. The novel DNA sequences and CC cancer or determining the risk of developing it and to screen for CC specific binding partners of the DNA or protein sequences, where the binding partners are potentially useful as agents for treating or CC diagnosing bronchial cancer. The DNA or protein sequences can also be used for prognosis, detection of metastases and for secondary treatment CC (of tumours that have been stabilised or are no longer detectable). CC Detecting abnormal expression of the DNA sequences provides early CC diagnosis of bronchial cancers. The present sequence is that of a novel bronchial cancer-associated human gene sequence of the invention.
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Best Local Sim
Matches 1229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid, and derived proteins, useful for diagnosis of bronchial cancer and in screening for therapeutic and diagnostic agents.
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P-PSDB; ADU06550.
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Li X, Roepcke
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                                                                                                                                                                                                                                                                                                 Sequence 4839 BP; 1103 A; 1313 C; 1290 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 285; 1381pp; German
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GGAAAGCTAGCGGCAGAGGCTCAGCCCCGGCGGCAGCGCGCCCCCGCTGCCAGCCCATT
                                                                             GGGCGCAGCGGAGCGCGGTCCCCGCGCGCACTGAGCCCCGGGGGAACTTGGCGGC
                                                                                                                                                                        GGGCGCAGCGGAGCGCGGTCCCGCGCACTGAGCCCCCGGGGAGCTTGGCGGC
                                                                                                              TTCCGGACGCCACCCGGGCACTGCCGACGCCCCGGGGCTGCCGAGGGGAGGCCGGGG
                                                                                                                                         ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                    93.0%;
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Hinzmann
                                                                                                                                                                                                                                         Mismatches
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Rosenthal
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, Pilarsky C;
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Matches 1229
                                                                                                                                                                                                                                                                                             The present invention relates to novel nucleic acid sequences that an expressed by human prostate cancer cells. The nucleic acid sequences the encoded proteins are useful as targets for treating, preventing and/or diagnosing cancers, particularly prostate cancer. The present sequence is one such nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid sequence that is expressed by cancer cells, useful as target for treating, preventing cancers, particularly prostate cancer.
                                                                                                                                                                                                                                                                             Sequence
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                                GGGCGCAGCGGAGCGCGCGCGCGCACTGAGCCCCGGGCGCCCCCGGGAACTTGGCGGC
                                                                                                                                                GGGCGCAGCGGAGCGCGGTCCCGCGCACTGAGCCCCGGGGCGCCCCCGGGAACTTGGCCGC
                                                                                                                                                                                  TTCCGGACGCCACCCGCGGGCACTGCCGACGCCCCCGGGGCTGCCGAGGGGAGGCCCGGGG
                                                                                                                                                                                                         SEQ ID NO 166; 198pp; English.
         CCGCCGGGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCA
                                                                 93.0%; Score 1229; DB 14; ilarity 100.0%; Pred. No. 7.2e-184; Conservative 0; Mismatches 0;
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RESULT 12
ADC37326
ID ADC37326
AC ADC37
XX ADC37
XX IB-DE
XX Nucle
             Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune dise cancer; infectious disease; bone disease; AIDS; neurodegenerative disease; ischaemic disorder; Antiinflammatory; Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HI Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene;
                                                                                                    Nuclear
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Matches 1228;
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05-DEC-2001;
03-OCT-2002;
04-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel proteins and their coding sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-kappaB). The proteins and their coding sequences are useful for treating a disease associated with NF-kappaB activation, such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases, or ischaemic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New purified protein that activates nuclear factor kappa B (NF. useful for treating inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseaschemic disorders.
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      TGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCA
                                  TGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGA
                                                   TGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGA
                                                                                          CCGCCGGGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCA
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2002JP-00291302.
2002US-0415769P.
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Pred. No. 1.4e-183;
0; Mismatches 1;
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(NF-kappaB)

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RESULT 13
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31-MAR-2003;
                       31-MAR-2004; 2004EP-00090124.
                                                                     EP1471075-A2
                                                                                             Homo sapiens
                                                                                                                     pancreas tumor;
                                                                                                                                             Pancreatic cancer associated human protein
                                                                                                                                                                    21-APR-2005
                                                                                                                                                                                            ADX97454;
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                                                                                                                     cytostatic;
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The invention relates to a novel human nucleic acid sequence of the comparises and its encoded protein. The invention further comprises: CC proteins and peptides, preferably isolated, that contain a sequence encoded by the novel nucleic acid; and methods for diagnosis and treatment of pancreatic cancer, using a substance that inhibits or binds content protein or its DNA, including: an antisense oligonucleotide, short interfering RNA or ribozyme directed against the pancreatic protein, an organic molecule, particularly having a molecular weight below 5000, and creatily 300, that binds to the pancreatic DNA, an aptamer or (monoclonal) antibody, preferably human or humanized, that binds to the pancreatic DNA, an aptamer or (monoclonal antibody, any of which may be derivatized with a reporter group, cytocoxic compound, immunostimulant and/or radioisotope. The novel human pancreatic proteins and their encoding DNA have cytostatic activity. The novel sequences are useful for inhibiting transcription and/or expression of genes and proteins associated with ancreatic cancer. This polymucleotide sequence represents the DNA encoding one of the novel shown in the specification, it has been electronically downloaded of office a DVD-rom provided with this specification by the Buropean Patent
 Matches 909;
                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosenthal A,
Lichtner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-768082/76.
P-PSDB; ADX97525.
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(ROSE/)
(PILA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid differentially expressed use as diagnostic agents and in screening
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(SPEC/)
                                                                  Sequence 4519
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ROSENTHAL A.
PILARSKY C.
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SPECHT T.
LICHTNER I
Conservative
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Staub E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO
                                                                  BP; 1074 A; 1162 C; 1169 G; 1114 T; 0 U; 0 Other
                 68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28pp; German.
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Roepcke S
 0
                 Score 909; DB 13;
Pred. No. 1e-133;
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 Mismatches
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Li X;
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                               Length 4519;
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RESULT 14
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 13-NOV-2001;
21-NOV-2001;
29-NOV-2001;
03-DEC-2001;
14-DEC-2001;
08-JAN-2002;
10-JAN-2002;
                                                                                                                                                                                                                    retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory;
                                                                                                                                                                                                                                                                                                      Cancer/angiogenesis/fibrosis-related nucleic
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                                                                                                                                                                                                                                                                                                                                                                                 ADN38809
                                                                                                            13-NOV-2002;
                                                                                                                                   22-MAY-2003
                                                                                                                                                           WO2003042661-A2
                                                                                                                                                                                                         vulnerary; gene therapy;
                                                                                                                                                                                                                                                          inflammatory disease; autoimmune disease;
                                                                                                                                                                                                                                                                    fibrotic disorder; psoriasis;
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2001US-0332464P.
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2002US-0347211P.
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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods a determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The conversion vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a conjugation of the invention; antibodies which specifically bind a conjugation of the invention; and antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and mucleic acids. The nucleic acids, polypeptides, concer and other conditions such as pooriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal convascularistation syndromes, scarring and uterine fibroids. They may sequence represents a nucleic acid sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2002;
20-FEB-2002;
29-MAR-2002;
04-APR-2002;
12-APR-2002;
15-JUN-2002;
16-JUL-2002;
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22-JUL-2002;
09-SEP-2002;
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Mack
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                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                             a nucleic acid in a
                                                                                                                                                                                                                                                                                            The invention
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2002US-03986614P.
2002US-0396839P.
2002US-0397845P.
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                                                                                                                                                                                                                                                                                             relates to nucleic acids and proteins
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Wilson F
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Œ, Zlotnik
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Sequence 864 BP; 173 A; 307 C; 254 G; 130

Query Match

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Score 864; DB 11; 1 Pred. No. 1.3e-126;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; con willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; cardiovascular disorder; ischemic heart disease; hydrocephalus;
                               08-SEP-2000
                                                                                                                                                              mat_peptide
                                                                                                                                                                                                                 sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                  brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder;
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The present sequence encodes a human TANGO 261 polypeptide. The CC specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular CC proliferation, modulate cellular differentiation and/or modulate cellular differentiation and/or modulate cellular differentiation and/or modulate cellular differentiation and/or modulate cellular differentiation, modulate cellular differentiation, modulate cellular cC adhesion, and cell traffishing and/or migration, modulate cellular cC adhesion, and cell traffishing and/or migration, modulate cellular cC cancer, modulate the proliferation, differentiation, and/or function of cC cancer, modulate the proliferation, and leukocytes, treat bone marrow, cC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial casthma and bronchiectasis, intestinal disorders, spleen associated cC diseases, modulate renal disorders, treat cardiovascular disorders such cC as ischemic heart disease, modulate the proliferation, differentiation, cand/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, cerebral codema, hydrocephalus, cc disease, multiple sclerosis, brain cancers, hydrocephalus and cc encephalitis, and treat hepatic diseases, hydrocephalus and cencephalitis, and treat hepatic disorders.
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Sequence 969 ВÞ; 211 A; 316 C; 294 G; 148 T; 0 Ġ, 0 Other;

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8 S 망 Ś 밁 á 밁 δ 맑 S 밁 F Matches Query Match Best Local 694 122 634 574 362 874 302 814 754 182 805; 62 N Similarity GGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAG 633 GCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCA CTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCG CCGGCACAGCCAGGGGCGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCC 693 GGTGGTGGTGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAG GGAGATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGATGATGGTGAT CGGGGAGGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCCGAGCA CCGGCACAGCCAGGGGGGGGGGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCC GCCCACCGACCGCCTGGCCGTGCCGCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCA CTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCG Conservative 60.8%; 0; Score 803.2; DB 3; Pred. No. 4.3e-117; 0; Mismatches 3; Indels 0; 813 121 61 933 361 873 301 241

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## SUMMARIES

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## ALIGNMENTS

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FEATURES BOUICE	COMPLEX	REFERENCE AUTHORS TITLE JOURNAL	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AL578575/c LOCUS DEFINITION
	Contact: Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Let strand cDNA was primed with a NotI-oligo(dT) primer: Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a sitistic of Tryitogen This sequence	Hominidae; Buther Buther Butter, Butter, Hominidae; Homo.  1 (bases 1 to 1005)  1 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  1 Full-length cDNA libraries and normalization  Unpublished (2001)  On Feb 16 2001 Hold semience version replaced q1:31316780.	AL578575 AL578575.3 GI:46257448 EST. Homo Bapiens (human) Homo Bapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Catarrhini;	AL578575 1005 bp mRNA linear EST 07-APR-2004 AL578575 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDNA clone CS0DK001YC24 3-PRIME, mRNA sequence.

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Pred. No. 8.7e-150;
9; Mismatches 10;
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Best Local Similarity 96.4%;
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Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:30492472.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-01igo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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AL517150
AL517150.3 GI:45653717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence belongs to sequence cluster 9945.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODA008CA12NP1&c=9945.r.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 1038)
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                                                     ACCGACCGCCTGGCCGTGCCGCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCC
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/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9666"
/clone="CS0DA008YB23"
/tissue type="YEUROBLASTOMA"
/tissue type="YEUROBLASTOMA"
/clone="The-"Homo sapiens NEUROBLASTOMA"
/clone="Twector: pCMVSPORT 6; 1st strand cDNA was primed
/note="Twector: pCMVSPORT 6; 1st prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Pred. No. 1.1e-149;
7; Mismatches 24;
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AGENCOURT_8287174 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6292265
5', mRNA sequence.
BQ641849
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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EST.
                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                               Hominidae; Homo.
1 (bases 1 to 967)
                                                                                                                                                                          cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                            organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"
                                                                                                    ocation/Qualifiers
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/clone_lib="NIH_MGC_43"
/note="organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies) Note: this is a NIH_MGC Library. | "
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Query Match Best Local Matches 771; Local Similarity 1184 1244 1064 1004 541 481 421 361 884 301 824 241 181 121 644 CAGGGGCGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGC 584 524 GAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTG 601 944 764 704 61 CGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTAT | CGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTAT ACAGTGTCAGGCAACCGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGAC ATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGC ATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGC GAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCGGGCTGGGG 1301 GGGACCCGGCTCCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGCAAA 1243 CACTACCCGGGGTCCTCCATCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAG 1183 TGCTACGGCAGCGGCGGCGCATGGAGGGGCCGCCCACCTACAGCGAGGTCATCGGC 1123 GATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACG 1063 CTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATG CCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCCGGGACCCCGAGCAGCAGCAGCTGGAA CCGTACCTGCAGCACGAGATCGACCTGCCGCCCACCATCTCGCTGTCAGACGGGGAGGAG | CCGTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAG ACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGAC GAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTG TGCTACGGCAGCGGCGTATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCGGC GATAGTGCCAGGCTGGGCGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACG CTGAACCGGGAGTCGGTGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATG CCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAA GGGACCCGGCTCCACCACACACACATCGCGCCCCTAGAGAGCGCAGCCATCTGGAGGCAA 720 CACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGAG Conservative 58.0%; 99.1%; 0 Score 766.8; DB 5; Pred. No. 1.5e-132; Mismatches Indels Length 0 Gaps 943 883 823 180 120 643 60 1003 300 240 763 703 660 600 540 480 360

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RESULT 4 BM922276 POCA?

DEFINITION BM922276 1046 bp AGENCOURT\_6707077 NIH\_MGC\_115 Homo 5', mRNA sequence. mRNA linear EST 12-MAR-2002 sapiens cDNA clone IMAGE:5754437

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KEYWORDS
SOURCE
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Location/Qualifiers
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Mammalia; Eutheria;
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="TMAGE:5754437"
/lab_host="DH10B"
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                                                                                                                                                                                                                             2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Email: seqref@genoscope.cns.fr eprime ist strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                     On Feb 15, 2001 this sequence version replaced gi:31265017.
Contact: Genoscope
Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae; Homo.

1 (Dases 1 to 1059)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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AL543170 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens
clone CSODI002YI03 5-PRIME, mRNA sequence.
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AL543170
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                                                                                                                                                               http://www.genoscope.cns.fr/cdna?s=CS0DI002AE02QP1&c=9945.r.
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                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                                                                                                                                            ocation/Qualifiers
                                          clone="CS0DI002YI03"
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WACCCCAATTTCTYCTTCACTTGTCTCAATTCAAACACTCTTTTTTCCATAACATGGAGA
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                    TGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCAGCAGTAACTCGG 1049
                                                                                          TGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACC
                                                                                                                                                                AGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGC
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                                                                      TGGAACTGAACCGGGAGTCGGTGSGKS--ACCCCAAACAGAWCCATCTTYGACAGTGACC
                                                                                                                                                                                                                  CCTATCCGTACCTGCAGCACGAGATCGACCTGCCGCCCACCATCTCGCTGTCAGACGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Direct Submission
Submitted (20-UUL-2004) Genoscope - Centre National
Submitted (20-UUL-2004) Genoscope - Centre National
Submitted (20-UUL-2004) Genoscope - Centre National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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1 (bases 1 to 901)
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/mol_type="mRNA"
/db_x=ref="taxon:9606"
/clone="csoD00105Y812"
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Pred. No. 9.5e-128;
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Conservative

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61

Query Match

Local Similarity

57.9%;

Score 764.2; Pred. No. 4.5 Mismatches

1.2; DB 1; 4.5e-132; ches 54;

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SOURCE
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                                                                                                                                                                                                                                                                        Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ954555
BQ954555.1 GI:22370033
EST.
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National Institutes of Health, M
Unpublished (1999)
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1 (bases 1 to 916)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                             e: LLAM13626 row: c column quality sequence stop: 669. Location/Qualifiers
/dev stage="adult, 70 yr"
/lab_host="DB10B"
/clone_lib="Lupski_sciatic_nerve"
/clone_lib="Lupski_sciatic_nerve"
/clone="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
/note: Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCTACACCGTCCG-3' and
5'-GACTACATCTCACATCGCGAGCGGCCGCCT(15)-3'. Size selected
1 kb for average insert length 1.87 kb. This is a priman
                                                                                                                   /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                              clone="IMAGE:6204609"
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library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. College of Medicine) and is available through Life
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CCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACG GCGCCGTCCATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGCCGGCGGGCAG асессеборого в поставорого в п GATAGTGCC-AGGCTGGGCGGCCCCTGCCCCCAGCAGTAACTCGGGCATCAG-CGCCA 1061 ATCACGTGCCTGAGGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGC GAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTG GAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTG CCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACG GCGCCGTCCATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGGCCAG ececceeccee Aececcecce de Contra de CGTGCTACGGCAGCGGCGGCC-GCATGGAGGGGCCGCCCCCCCCACCTACAGCGAGGTCATC 1120 GATAGTGCCAAGGCTGGGCGGCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCCGCCA CTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATG 1003 CCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAA CCGTACCTGCAGCACGAGATCGACCTGCCACCCACCCATCTCGCTGTCAGACGGGGAGGAG CGCCTGGCCGTGCCGCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTAT CAGGGGCGAGGAGAAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCCTCGGAGAGC 703 CTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATG CCCCCACCCTACCAGGCCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAA CCGTACCTGCAGCACGAGATCGACCTGCCGCCCACCATCTCGCTGTCGGACGGGAGGAG CGCCTGGCCGTGCCGCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTAT ACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGAC ACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGAC CAGGGGCGGAGGAGAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGC ATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACAGC CGTGCTACGGCAGCGGGGGGGCATGGAGGGGGGGGGGCGCCCCCTACACCGAGGTCAAT 780 Conservative Technologies." 55.7%; 95.7%; , , Score 736.4; DB 5; Pred. No. 6.8e-127; Mismatches Indels Length 5 Gaps (Baylor 943 540 643 463 60 360 240 660 883 480 823 420

AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORM HOMO sapiens CDNA clone CSODJ015YF12 3-PRIME, mRNA sequence. AL558881 linear EST 02-APR-2004 LINE) COT 10-NORMALIZED

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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31283014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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EST.
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Location/Qualifiers
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ATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCC 1060
                                                                                                                                      GAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCAGCTG 940
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/cell_type="T CELLS (JURKAT CELL LINE)
/cell_line="JURKAT"
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/db_xref="taxon:9606"
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Pred. No. 1.8e-126;
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Local Similarity 96.2%;
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30378625
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http://www.genoscope.cns.fr/cdna?s=CSODJ014CG08NP1&c=9945.r.
Location/Qualifiers
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                                                                                          /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                            /clone="CSODJ014YN15"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
                                                                                                                                                                                                                                                                     organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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; Pred. No. 6.5e-123;
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Query Match

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AL558882 Homo sapiens T C
Homo sapiens cDNA clone C
AL558882
AL558882.3 GI:46184269
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) On Feb 15, 2001 this sequence version replace Contact: Genoscope
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                  Hominidae, Homo.
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CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
CSODJ015YF12 5-PRIME, mRNA sequence.
               version replaced
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                                                                                                 ACGTGCTACGGCAGCGGCGCGCATGGAGGGGCCGCCCCACCTACAGCGAGGTCATC
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Query Match
Best Local Similarity
Matches 736; Conserv
                                                                                                                                   581 GTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For more information about this cluster, see http://www.genoscope.cns.fr/cdna7s=CSODJ015DC06QP1&c=9945.r.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   division of Invitrogen. This sequence belongs to sequence cluster
AGCCAGGGGCGGAGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAG
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                  /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR vsites of the pCMVSPORT 6 vector. Library was normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="teaxon:9606"
/db_xref="teaxon:9606"
/clone="CSODJ015YF12"
/cell_type="T_CELLS (JURKAT_CELL LINE) COT 10-NORMALIZEI
/cell_line="JURKAT"
/clone_lib="Homo sapiens T_CELLS (JURKAT_CELL LINE) COT
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                                                                                                                                                                                                           Score 714.6; DB 1;
Pred. No. 7.8e-123;
2; Mismatches 1;
                                                                                                                                                                                                                     Indels
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TITLE
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Best Local Similarity
Matches 764; Conserv
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2757 row: p column: 18
High quality sequence stop: 663.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BU539219 945 bp mRNA linear ES' AGENCOURT 10215265 NIH MGC_107 Homo sapiens cDNA clone IMAGE:6569922 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.
1 (bases 1 to 945)
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                              GGTGATGATGGTGATGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGC
  GGTGATGATGGTGATGGTGGTGATCACGTGCCTGAGCCACTACAAGCTGTCTGC
                                                                                                                                                                                             TCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="adenocarcinoma, cell line"
/lab_host="blide" (hage-resistant)"
/lab_host="blide" (hage-resistant)"
/clome_lib="NIH_MGC_107"
/clome_l
                                                                                                                                                                                                                                                                                          Conservative
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/mol_type="mRNA"
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93.7%;
                                                                                                                                                                                                                                                                                        Score 691.2; DB 5;
Pred. No. 1.8e-118;
0; Mismatches 44;
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AGENCOURT 10016502 NIH MGC 142 Homo sapiens
IMAGE:6497853 5', mRNA sequence
BU602918
     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM2679 row: i column: 22
                                                                                                                                                                                                                                               1 (bases 1 to 850)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                         CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation DNA Sequencing by: Agencourt Bioscience Morgania Corporation Can be Clone distribution: MGC clone distribution information can be
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Location/Qualifiers
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CAGTGGGCCG-CCCTCCTTGCTGG-AGGGGACCCGGCTCCACCACACACACACACCGCCC 1216
                                              AACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_libe="NHH MGC 142"
/clone_libe="NHH MGC 142"
/note="Vector: \( \overline{DNR}\)-LIB; Site_1: SfiI (ggcattatggcc);
/note="Vector: \( \overline{DNR}\)-LIB; Site_1: SfiI 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used in cloning as follows:
5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
5'-ATTCTAGAGGCCGAGGCGGCGAGTGGCCATTACGGCCGGG-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the >0.5 k
size fraction (other fractions present in NIH_MGC_141).
Library created in the laboratory of M. Brownstein (NIMH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH). Note: this is a NIH_MGC Library."
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db_xref="taxon:9606"
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Query Match
Best Local Similarity
Matches 651; Conserv
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 780)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            These sequences were made by sequencing genomic exons and ordering them based on alignment.
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Science 302 (5652),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-NOV-2003) Celera Genomics,
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Mammalia; Eutheria;
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                                           GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG
                                                                                                                                        GCCAGGGGCGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA 701
                                                                                                                                                                                   TGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA
                                                                                                                                                                                                                                                                               CGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGG
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="TMEPAI"
/locus_tag="HCM6856"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                     Score 651; DB 10;
Pred. No. 5.3e-111;
0; Mismatches 104;
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TRANSCRIPT, partial sequence,
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Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., LLiu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.
High-throughput cloning of full-length human cDNAs directly
OriGene Technologies, Inc. 6 Taft Ct. Suite 100 Rockville, MD 20850
                                                    Email: cDNA@origene.com
This EST submission is part of an on-going human full-length
cloning project at Origene Technologies, Inc.
Please contact Origene for access.
                                                                                                       Contact: Kovacs, KF
High Throughput cDNA Cloning
OriGene Technologies, Inc. ( www.origene.com )
OriGene Technologies, Inc. ( www.origene.com )
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
Email: CDNA@origene.com
                                                                                                                                                                                                                                         CDNA libraries optimized for large and rare transcripts Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DN992322 647 bp mRNA linear EST 17-MAY-2005 TC124411 Human adult whole brain, large insert, pCMV expression library Homo sapiens cDNA clone TC124411 5' similar to Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript
                                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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FEATURES
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Seg primer: pCMV6 5prime
Technologies Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="Whole brain"
/clone Tib="Human adult whole brain,
expression library"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC124411"
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ATGGTGATGGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCC 625		GCCGCCGCCGCCGGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTC 505	GCCCCGCGCCGCCGCGCCGCGCCGTCCATGCACCGCTTGATGGGGGTCAACAGCACCGCC 445	GCGGGGCCCCAGCTCCGGGCGCGGGCCGGAGCCCCCCGGGCCGCCCGAGCCCCCGGC 385	TGGCGGCGACCCGAGGCCCGGCGAGCCGGGGGCGCCTCCCCCGCCGCCGCCGCCCTCCTGCAT 325	48.0%; Score 634.2; DB 7; Length 711; Similarity 93.2%; Pred. No. 7.2e-108; 3; Conservative 0; Mismatches 48; Indels 0; Gaps 0;	/organism="Sus scrofa" /mol_type="mRNA" /db_xref="taxon:9823" /clone="Tct01F020083" /clssue_type="trachea" /dev_stage="adult" /clone_lib="full-length enriched swine cDNA library, adult trachea"	(conal (cenoda : +81- : +81- il: hu proje mal Ge obiolo jle pa gle pa rary rary cor se cross	14881463 Contact: Hirohide Uenishi Animal Genome Laboratory, Genome Research Department	Okumura, N., Hamasima, N. and Awata, T. PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries Nucleic Arids Res. 32 (1). D484-D488 (2004)	lls. (bases 1 to 711) nishi.H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,	EST.  Sus scrofa (pig) Sus scrofa Ext.  Sus scrofa Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;	ll-length clone TCH

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Search completed: February 28, 2006, 12:21:53 Job time : 6118.44 secs

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Issued_Patents_NA:*

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2: /cgn2_6/ptodata/l/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/l/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/l/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/l/ina/H_COMB.seq:*

6: /cgn2_6/ptodata/l/ina/PC_COMB.seq:*

7: /cgn2_6/ptodata/l/ina/PC_COMB.seq:*

8: /cgn2_6/ptodata/l/ina/RE_COMB.seq:*

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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67.6	67.6	67.6	67.6	67.6	68	68	68.4	68.4	68.8	69.4	70.4	71.8	72.2	72.2	75.4	75.4	90.4		351.6	352.2	352.2	755.8	801.6	Score		
5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.2	5.2	5.2	5.3	5.3	5.4	5.5	5.5	5.7	5.7	6.8	21.5	26.6	26.7	26.7	57.2	60.7	Match		ď
12001	4257	4257	4257	4257	44377	44377	152145	152132	4411529	13343	4403765	40586	2561	2561	2561	2561	391	867	937	8065	921	759	1140	Length		
N	w	ω	w	N	N	N	w	w	w	w	w	w	w	w	w	w	ω	ω	w	w	w	w	w	88		
US-08-458-568A-11	US-09-825-288A-1	US-08-843-659-1	US-09-259-821A-1	US-08-690-473-1	US-08-804-198-1	US-08-804-227C-7	US-09-949-016-12371	US-09-949-016-13845	US-09-103-840A-1	US-09-949-016-17015	US-09-103-840A-2	US-09-949-016-16965	US-09-976-740-48	US-09-616-289-48	US-09-976-740-48	US-09-616-289-48	US-09-621-976-2162	US-09-091-952A-8	US-09-311-021-65	US-09-091-952A-6	US-09-091-952A-7	US-09-769-482-2	US-09-769-482-1	,ID		
Sequence II, Appl	Sequence 1, Appli	Sequence 7, Appli	Sequence 12371, A	. Sequence 13845, A	Sequence 1, Appli	Sequence 17015, A	Sequence 2, Appli	Sequence 16965, A	Sequence 48, Appl	•	Sequence 48, Appl	Sequence 48, Appl	Sequence 2162, Ap	Sequence 8, Appli	Sequence 65, Appl	Sequence 6, Appli	•	Sequence 2, Appli	Sequence 1, Appli	Description	•					

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	. 27	26	25
63.4	63.6	64	64	64	64	. 64	64.4	64.4	64.4	64.4	65	65.4	65.4	65.4	66	66.6	66.6	66.6	66.6	67
4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.9	4.9	4.9	4.9	4.9	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.1
10745	9984	4524	4524	4524	3492	1206	12425	12425	1614	1614	5871	4403765	670690	670689	152331	12425	12425	1614	1614	4411529
w	w	w	ω	N	ω	w	ω	w	w	w	w	w	ω	w	w	w	w	w	w	Į,
US-09-949-016-16940	US-09-949-016-13283	US-09-430-854-7	US-09-206-537-7	US-08-845-998-7	US-09-949-016-837	US-09-949-016-5866	US-09-976-740-50	US-09-616-289-50	US-09-976-740-45	US-09-616-289-45	US-10-152-886-24	US-09-103-840A-2	US-09-949-016-14207	US-09-949-016-12505	US-09-128-155-16	US-09-976-740-50	US-09-616-289-50	US-09-976-740-45	US-09-616-289-45	US-09-103-840A-1
Sequence 16940, A	Sequence 13283, A	Sequence 7, Appli	Sequence 7, Appin	Sequence 7, Appli	Sequence 837, App	Sequence 5866, Ap	Sequence 50, Appl	Sequence 50, Appl	Sequence 45, Appl	Sequence 45, Appl	Sequence 24, Appl	Sequence 2, Appil	Sequence 14207, A	Sequence 12505, A	Sequence 16, Appl	Sequence 50, Appl	Sequence 50, Appl	Sequence 45, Appl	Sequence 45, Appi	sequence 1, Appli

## ALIGNMENTS

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							Query Match Best Local Matches 80	ÚS-09-769-482-	LOCATION:	FEATURE:	ORGANISM:	TYPE: DNA	LENG	SEQ ID	SOFTWARE:	NUMBER OF	SO TOR	PRIOR		CURRENT		PILE S		APPLICANT:	APPLICANT:	APPLICANT:	GENERAL INFORMATION:	Patent No.	); Sequence 1,	OLT 1
694	211	634	151	574	91	514	Match ocal Si	9-482	ION:	RE:	NISM:	DNA	LENGTH: 1140	$\vdash$			RTT.TNG	FILING	APPL			EFERI		:TNA:	ANT:	TNA	L LNFC		1.	
CTCGG	ccesc	ccec	GGTGGTGGTGATCACGTGCTGATCAGGCCACTACAAGCTGTCTGCACGGTCCTTCATCAG	GGTGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAG	GCCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGAT	GGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGATGGTGAT	₽.		(95)(850)	3	Homo		40		PatentIn Ver.	SEO ID NOS: 67	REFLICATION MONDEN: 00/1/0/010	CATTON		FILING DATE:	APPLICATION NUMBER: US/09/769,482	REFERENCE: 04995.0057-00000	INVENTION:	SEGAWA,	XU,	MOUL	SRIVASTAVA	6566130	Application US/09769482	_
GGAGAGCACAG	ACAGO	ACAGO	TEGTE	reere	reece	TCACG	60. larity 99. Conservative		. (850		sapiens				In Ve	NOS:	20	NI NI NI	NUM	ATE:	ION N	04995			XU, LINDA L.	MOUL, JUDD	TAVA		catio	
ACAGT	CAGGG	CAGGG	ATCAC	ATCAC	GAGCT	GAGCT	60.7%; 99.5%; ative		_		as				2	67	DATE: 2000-01-31	/03 - 01-28	BER:	2001	UMBER	. 0057	ROSTA	TAKEHIKO	F	_	SHTV		NS/	
STCAGO	GCGGAC	GCGGA	STGCC	FIGCC	GAGT	GAGT	0								_	,	31	-28	50/178	2001-01-26	: US/C	-0000	14047. 140-11	6		•	7		97694	
CTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCGGCCTCG	CCGGCACAGCCAGGGGCGGAGGAGAAGATGCCCTGTCC	CCGGCACAGCCAGGGGGAGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCC	GCTGA	GCTGF	TGIT	TGTT	2 2										,	045	3,772		9/769		PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED PROVINCIAGOTTE ARRAY					•	82	
GAATO	AAGAT	AAGAT	GCCAC	AGCCAC	AGATO	AGATO	ore 801.6; ed. No. 5.3 Mismatches														,482		PANUX							•
CCAGA	GCCCT	GCCCT	TACAA	TACAA	ATCAT	ATCAT	.6; DB 3; 5.3e-142; ches 4;																OGEN-							
GCCGC		GICCI	GCTGT	GCTGT	CATC	CATC	42;																STGNA							
AGGTC	TCAGAAGGATGCCTGTGGCC	CAGAA	CTGCA	CTGCA	reere	regre	Length Indels																TING-							
TACGC	GGATG	GGATG	CGGTC	CGGTC	GTGAT	GTGAT	114																ASSOC							
CCCGC	CCTGT	CCTGT	CTTCA	CTTCA	GATGG	GATGG																	TALED							
		-			_	_	Gaps																							
753	270	693	210	633	150	573	0;					•																		

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APPLICANT: SEGAWA, TAKEHIKO

APPLICANT: SEGAWA, TAKEHIKO

TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

TITLE OF INVENTION: POYNUCLEOTIDE ARRAY

FILE REFERENCE: 04995.0057-00000

CURRENT APPLICATION NUMBER: US/09/769,482

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/178,772

PRIOR APPLICATION NUMBER: 60/179,045

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 2

LENGTH: 759

TYPE: DNA

CORGANISM: Homo sapiens

US-09-769-482-2
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US-09-769-482-2
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APPLICANT: SRIVASTAVA, SHIV
APPLICANT: MOUL, JUDD W.
APPLICANT: XU, LINDA L.
                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09769482 Patent No. 6566130
              Best Local Similarity Matches 757; Conserv
                                        Query Match
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              Conservative
                         57.2%;
99.7%;
              0,
            Score 755.8; DB 3;
Pred. No. 2.1e-133;
0; Mismatches 2;
              Indels
                                       Length 759;
              0
              Gaps
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US-09-091-952A-7
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                                                                                                                                                                                                     Sequence 7, Application US/09091952A Patent No. 6458532
GENERAL INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
STREET: Two Embarcadero
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                        1118
                                                       NUMBER OF SEQUENCES:
                                                                                                                                                              APPLICANT: Detera-Wadleigh,
Gershon, Elliot;
Badner, Judith A
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                                                    Hauner, Tynn R.
Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Esterling, Lisa E.
Esterling, Lisa E.
TINVENTION: Chromosomal Markers and Diagnostic
Tests for Manic-Depressive Illness
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                                                                                                                                                                                           Sevilla
                Townsend and Crew LLP
Center, Eighth Floor
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US-09-091-952A-7
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FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-3834
COMPUTER READABLE FORM:
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LOCATION: 1...921
OTHER IMPORMATION: Clone 2:
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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CCCGAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATC 985
                                                                                                                                 CGCTTCCAGCCCACCTACCCCTATGTGCAGCACGAGATTGATCTTCCTCCCACCATCTCC
                                                                                                                                                                      GCCCCGCGGTCCAGGGACAGGTTCACAGCGCCCGTCCTTCATCCAGAGGGATCGCTTCAGC
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/091,952A FILING DATE: 19-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                CTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGAC 925
                                                                                                                                                                                                                                            ACGGTGATGGTGGTCATCGTCTGCCTGCAACCACTACAAAGTCTCCACGCGGTCC
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73.1%;
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US-09-091-952A-6
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                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
PILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
PILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-199
CLASSIFICATION: <Unknown>
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 8065 base pairs
TYPE: nucleic acid_
                                                                                                                                                                                                                                                                                               NAME: Smith, Timothy L. REGISTRATION NUMBER: 35,31 REPERENCE DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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MEDIUM TYPE: Diskette
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                   FEATURE:
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                                                                                                   FEATURE:
                                                                                                                          MOLECULE TYPE:
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NAME/KEY:
                                                                                NAME/KEY:
                                                                                                                                                          STRANDEDNESS: single
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Gershon, Elliot
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Yoshikawa, Takeo
Sanders, Alan R.
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; NAME/KEY: misc feature
LOCATION: 5595...5685
; LOCHIER INFORMATION: amplified
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-091-952A-6
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Sequence 65, Application US/09311021
Patent NO. 6706869
GENERAL INFORMATION:
APPLICANT: Wong, Gordon G.
APPLICANT: Fechtel, Kim
APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Agostino, Michael J.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING
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LOCATION: 452...505
OTHER INFORMATION: alternatively
FEATURE:
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OTHER INFORMATION:
FEATURE:
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73.1%;
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Pred. No. 2.6e-57;
0; Mismatches 168;
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US-09-091-952A-8 RESULT 6

Sequence 8, Application US/0909195; Patent No. 6458532 PATENT INFORMATION: APPLICANT: Detera-Wadleigh,

US/09091952A

Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
Gerrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Esterling, Lisa E.

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; SOFTWARE: PatentIn V
; SEQ ID NO 65
; LENGTH: 937
; TYPE: DNA
; ORGANISM: Homo sapi
US-09-311-021-65
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/311,021
CURRENT FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 268
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                                                                            TAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGGGGGCGATGGAGGGGGCGGCGCC 110:
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               GCTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGA
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 CACATACAGCGAGGTGATGGGCCACCACCCAGGCGCCTCTTTCCTCCATCACCAGCGCAG
                                                      CAACTCGGGCATCAGTGCAAGCACCTGCAGCAGTAACGGGA
                                                                                                          CCGCTTCCAGCCCACCTACCCCTATGTGCAGCACGAGATTGATCTTCCTCCCACCATCTC
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73.0%;
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Pred. No. 2.4e-57;
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Matches 453;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                 166
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              346
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                     CTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCC 745
                                                                                                                                                                                                                      TTCATCAGCCGGCACAGCCAGGGGGGGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGC 685
                                                                                                                                                                                                                                                              ACGGTGATGGTGGTCATCGTCTGCCTGCTGAACCACTACAAAGTCTCCACGCGGTCC
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OTHER INFORMATION: C:
spliced coding region
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/091,952A FILING DATE: 19-Apr-1999 CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                           TTCATCAACCGCCCGAACCAGAGCCGGAGGCGGGGAGGACGGGCT---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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015280-297100US
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                                                                                         GENERAL INFORMATION:
                                  APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
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; NAME/KEY: CDS
; LOCATION: 17..223
US-09-621-976-2162
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                                 US-09-616-289-48/c
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                                                     RESULT 8
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SOFTWARE: Patent.pm
SEQ ID NO 2162
Sequence 48, Application US/09616289 Patent No. 6632923
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 112; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo &
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: GENSET 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dumas Milne
APPLICANT: Jobert, S.
APPLICANT: Giordano, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ESTs and Encoded Human Proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGTCAGACGGGGAGGAGCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGAC 925
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                                                                                                                                                                                                                 GGGCGCATGGAGGGGCCGCCCCCCCCCCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCC 1138
                                                                                                                                                                                                                                                                         ACATACAGCGAGGTGATGGGCCACCACCCAGGCGCCTCTTTCCTCCATCACCAGCGCAG
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                                                                                                           TCTTTCCTCCATCACCAGCGCAGAACGC 173
                                                                                                                                            TCCTTCCAGCACCAGCAGCAGCAGTGGGC 1166
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75.7%;
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CANT: Arjona, Anibal A. OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

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; LOCATION: (24)
US-09-616-289-48
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PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASCESQ for Windows Version 4.0
SEQ ID NO 48
                                                                                                                                                                                     GENERAL
                                                                                                                                                                                                                    Sequence
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Best Local Similarity
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
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TYPE: DNA
ORGANISM: Oryctolagus
FEATURE:
                                                                                                                                                                                     INFORMATION:
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ilarity 53.0%;
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                  FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
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APPLICATION NUMBER: US

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PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                            GENERAL INFORMATION:
                                                                                                                           Sequence 48, Application Patent No. 6632923
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W. A.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
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LOCATION: (246)...(1895)
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Local Similarity 53.0%;
es 206; Conservative
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Pred. No. 2.7e-05;
0; Mismatches 181;
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NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASESEQ for Windows
SEQ ID NO 48
LENGTH: 2561
                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 48 LENGTH: 2561
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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LOCATION: (246)...(1895)
                                                                                                                                                   TYPE: DNA
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                                                                                                         ORGANISM: Oryctolagus
NAME/KEY: CDS
LOCATION: (246)...(1895)
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for Windows Version 4.0
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Pred. No. 0.00011;
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Matches
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                 Matches 166;
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/241,755
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TYPE: DNA
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Local Similarity 51.4%;
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Pred. No. 0.00019;
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Pred. No. 0.00011;
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UMBER: US/99/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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SEQ ID NO 2
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Best Local Similarity
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OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND
FILE REFERENCE: CL001307
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182;
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GAGCCCGGAGGAGCCCGGCGCACCTCGCGCGGCGGCCGCTCCCGGCTGGAGC 279:
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                                                                                     GAGCCGGGGCGCCTCCCCCCGCGCGCGCCCTCCTGCATGCGGGGCCCCAGCTCCGGGCG
                                                                                                                                                                                                                                                                                                                                                                GAGGACGCCCGCACCCCTTCCCCCGCGCCCGCGGCGCCCCTGCGGGGGCCGGGGACCCCGGGA 2680
                                                                                                                                                                                     AAGGCGCGCGGTGGGGGGAGGGGGCGCAGCTGCGGCGAGCGCGAGTTGTGCACCCGGCG
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Pred. No. 0.00045;
0; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 13343;
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NESULT 15
US-09-103-840A-1
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; Patent No. 6294328
; Patent No. 6294328
; Patent No. 6294328
; Patent No. Franciscurian, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: WHITE, Owen R.
; APPLICANT: PRASER, Claire M.
; APPLICANT: PRASER, John C.
; APPLICANT: VENTER, John C.
; APPLICANT: PRASER, JOHN SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION UNDER: US/09/103,840A
; CURRENT APPLICATION UNDER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOOTWARE: PatentIn Ver. 2.1
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; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
Search completed: February 28, 2006, 12:29:25 Job time : 273.59 secs
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                                                                                                                                                                                                             3943088 GCCTCTCAGCTACCAACGGCGGCAGCGGCGCCGG--CGGCACCGGAGGCGACGGCG 3943145
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                                                                                                        3943206 GCGGACAAGGTGGCCAGGGCGGCGGCGGCGGTGCCGG 3943245
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                                                                                                                                                                                                                                                               240 CTGAGCCCCGCGGCGCCCCCGGGAACTTGGCGGCGACCCGAGCCCGGCGAGCCGGGGCGC 299
                                                                                                                                              420 GCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 GGCGGCGGCGGCGGAGGCGCTCGGCTGGGGAAAGCTAGCGGCAGAGGCTCAGCCCCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GACCGCGGTCTCGGAGCGAAACCCGATCTCCTTGGACTTGAATGAGGAGGAGGAGGAGGCGGC 61
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Run on:

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Total number of hits satisfying chosen parameters:
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10: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
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US-10-269-909-85
US-10-872-972-119
US-10-872-972-119
US-10-872-972-119
US-10-872-973-52
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Biocceleration Ltd.
Sequence 1, Appli
Sequence 84, Appl
Sequence 85, Appl
Sequence 119, App
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Sequence 300, App
Sequence 301, App
Sequence 217, App
Sequence 25, Appli
Sequence 412, App
Sequence 412, App
Sequence 44, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lee, I
APPLICANT: Lands
APPLICANT: Turi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Matches 1321;
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1321; DB 3; Best Local Similarity 100.0%; Pred. No. 4.5e-310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (413)...(1273)
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                                                                                                                                                                                                                                                                                                                                   1 CGACCGCGGTCTCGGAGCGAAACCCCGATCTCCTTGGACTTGAATGAGGAGGAGGAGGAGGCGG
                                                                                     CGACCGCGCTCTCGGAGCGAAACCCCGATCTCCTTGGACTTGAATGAGGAGGAGGAGGCGG
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US-10-343-479-2
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US-09-934-249-14
US-09-934-249-167
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Sequence 13108, A
Sequence 20307, A
Sequence 20, Appl
Sequence 197, App
Sequence 16, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45, Appli
Sequence 2, Appli
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Sequence 12, Appl
Sequence 32, Appl
Sequence 14, Appl
Sequence 11, Appl
Sequence 11658, A
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Sequence 1023, Ap
Sequence 1228, Ap
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

Minimum DB Maximum DB

seq length: 0 seq length: 2000000000

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Title: Perfect score:

US-09-934-249-1 1321

Result No.

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1229 1229 1229 1229 1229 1229 861 861 803.2 802.2 802.2 802.2 802.2 802.2 802.2 802.2 802.2 767.4

4839 4839 4839 4839 864 861 961 1141 1141 1141

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Gaps

240

180 120 120 60 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATCATCATCGTGGTGGTGATGGTGATGGTGGTGATCACGTGCCTGCTGAG
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APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Polakis, Paul
APPLICANT: Polakis, Paul
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Zhang, Zemin
ITITE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
ITITE OF INVENTION: TREATMENT OF TUMOR
ITITE OF INVENTION INVEST: US/10/241, 220
CURRENT APPLICATION NUMBER: US/10/241, 220
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 119
LENGTH: 4839
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; ORGANISM: Homo
US-10-241-220-119
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US-10-241-220-119
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Best Local Similarity
Matches 1229; Conserva
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APPLICANT: HUMBAN, RALPH H.

APPLICANT: ARGANI, PEDRAM

APPLICANT: ARGANI, PEDRAM

APPLICANT: MACTOR, WAITENAN

TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES

FILE REFERENCE: 58303(71699)

CURRENT APPLICATION NUMBER: US/10/269,909

CURRENT FILING DATE: 2003-10-11

PRIOR APPLICATION NUMBER: 60/328,609

PRIOR APPLICATION NUMBER: 60/328,609

PRIOR FILING DATE: 2001-10-11

PRIOR PILING DATE: 2001-11-19

NUMBER OF SEQ ID NOS: 87

NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-10-269-909-84
; Sequence 84, Application US/10269909
; Publication No. US20030180747A1
; GENERAL INFORMATION:
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                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-269-909-84
                                                                                                         SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 84
Query Match
                                                                                            LENGTH: 4839
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   93.0%;
   Score 1229;
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	•	Best Loc Matches
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1 GAAAAGCTAGCGGCAGAGGCTCAGCCCCGGCGGCGCGCGC	93 GGAAAGCTAGCCGCAGAGGCTCAGCCCCGGCGGCGCAGCGCCCCGCCGCCGCCCGC	Best Local Similarity 100.0%; Pred. No. 8.9e-288; Matches 1229; Conservative 0; Mismatches 0;
CG CG	-ccc	, 8, 1
CCCCCT	CCCCGCT	288; 0; Indels 0; Gaps 0;
GCCAG	GCCAC	0;
CCCATT	CCCATT	Gaps
60	152	0;

1172	1113 AGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGAGCAGTGGGCCGCCCT	Ş
; 1112 ; 1020	53 TCAGCGCCACGTGCTACGGCAGCGGCGGCG 	유 성
1052	993 GTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCCGGCAGTAACTCGGGCA	유
992		A 4
932	873 ACGGGAGGAGCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGC	B 6
9 872 9 780	3 AGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCACCCAC	β <b>δ</b>
812	753 GGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCC	B &
660	93	B &
692	633 GCCGGCACAGCCAGGGGCGGAGGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGC	B 8
540	73 81	B &
. <b>572</b>		B &
r) 4.	3 CCGCC	음 성
360	5 TO	음 성
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332	73 GACCCGAGCCCGGCGAGACCGGGGGGGGGCGCCCCCCGCCG	음 성
180	13 GGGC       21 GGGC	B 5
120	153 TTCCGAACGCCACCCGCGGGCACTGCCGACGCCCCCGGGGCTGCCGAGGGGAGGCCGGGGGACGCCGCGGGGTTGCCGACGCCGACGCCCCCGGGGCTGCCGACGCCGACGCCCCCGGGGCTGCCGAGGGAAGGCCGGGGGACGCCCCCGGGGGACGCCCCCGGGGGACGCCGACGCCGACGCCGACGCCGACGCCGACGCCGACGCCGACGCTGCCGAACGCCGACGCTGCCGACGGGAAGGCCGGGGGACGCCCCCGGGGGACGCCCGACGCTGCCGACGGAAGGCCGACGCACGC	B 22
152	93 GGAAAGCTAGCGGCAGAGGCTCAGCCCCGGCGGCGGCGGCGCGCCCGGCTGCCAGCCCATT	9 X

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Sequence 85, Application US/10269909

Publication No. US20030180747A1

GENERAL INFORMATION:
APPLICANT: HRUBAN, RALPH H.
APPLICANT: ARGANI, PEDRAM
APPLICANT: IACOBUZIO-DONAHUE, CHRISTINE
APPLICANT: IACOBUZIO-DONAHUE, CHRISTINE
APPLICANT: IACOBUZIO-DONAHUE, CHRISTINE
APPLICANT: IACOBUZIO-DONAHUE, CHRISTINE
APPLICANT: MAITRA, ANIRBAN
CURRENT: INTERNAMINA ANIRBAN
CURRENT APPLICATION NUMBER: US/10/269,909

CURRENT APPLICATION NUMBER: 60/328,609

PRIOR APPLICATION NUMBER: 60/328,609

PRIOR APPLICATION NUMBER: 60/328,754

PRIOR APPLICATION NUMBER: 60/332,754

PRIOR FILING DATE: 2001-11-19

NUMBER OF SEO ID NOS: 87

SOFTWARE: PatentIn Ver. 2.1

SEO ID NO 85

LENGTH: 4839

TYPE: DNA
ORGANISM: Homo sapiens
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                                         CCGCCGGGCAGCCCAATGTCTCCTGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCA
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  TGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGA
                                                                                   GCCGCGCCGCCGCCGTCCATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCG
                                                                                                                                           CCCAGCTCCGGGCGCCGGAGCCCCCCCGGCCGCCCGAGCCCCCGGGGCCCCGC
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US-10-872-972-119
                                                                                   APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Micke
                                                                                                                                                                     Sequence 119, Application US/10872972 Publication No. US20040229277A1 GENERAL INFORMATION:
 APPLICANT: Wu, Thomas
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: PSOLORI-US
CURRENT APPLICATION NUMBER: US/10/872,972
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CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/10/241,220
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 119
LENGTH: 4839
TYPE: DNA
ORGANISM: Homo Sapien
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APPLICANT: Zhang, Zemin

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: TREATMENT OF TUMOR

FILE REPERENCE: P5010R1-US

CURRENT APPLICATION NUMBER: US/10/872,991

CURRENT FILING DATE: 2004-06-21

PRIOR APPLICATION NUMBER: US/10/241,220

PRIOR FILING DATE: 2002-09-11

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 119

SEQ ID NO 119

LENGTH: 4839

TYPE: DNA

ORGANISM: Homo Sapien

US-10-872-991-119
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Publication No. US20040242860A1
GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: phillips, Heidi
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APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER

TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TRE

TITLE OF INVENTION: RHEUMATOID ARTHRITIS

FILE REFERENCE: 10872.51496

CURRENT APPLICATION NUMBER: US/10/287,436A

CURRENT FILING DATE: 2002-10-31

PRIOR APPLICATION NUMBER: US 60/336,220

PRIOR FILING DATE: 2001-10-31

NUMBER OF SEQ ID NOS: 1446

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 300

LENGTH: 4839

TYPE: DNA

ORGANISM: Homo sapiens

US-10-287-436A-300
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Latson, Susan R.

Eos Biotechnology, Inc.

Eos Biotechnology, Inc.

INVENTION: Methods of Diagnosis of Cancer, Compositions and Methods of Streening for Modulators of Cancer

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               APPLICATION NUMBER: US 60/355, FILING DATE: 2002-02-08
APPLICATION NUMBER: US 60/356,
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: 2002-02-08
NUMBER: US 6
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                     60/356,714
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NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 127
LENCTH: 864
TYPE: DNA
CRGANISM: Homo sapiens
US-10-295-027-127
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Sequence 3, Application US/09934249

Patent No. US20020115081A1

GENERAL INFORMATION:

APPLICANT: Lee, Richard T.

APPLICANT: Lae, Richard T.

APPLICANT: Turi, Thomas G.

APPLICANT: Thompson, John F.

APPLICANT: Kennedy, Scott P.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS

FILE REFERENCE: P0738/7001/ERP/KA

CURRENT APPLICATION NUMBER: US/09/934,249

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 60/227,159

PRIOR APPLICATION NUMBER: US 60/227,159

PRIOR APPLICATION NUMBER: US 60/227,159

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 17

SOFTWAARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 3
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TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(861)
S-09-934-249-3
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Best Local Similarity 100.0%; Pred. No. 1.1e-198;
Matches 861; Conservative 0; Mismatches 0;
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	NUMBER: 09/599,596: 2000-06-22	FILING DATE:	PRIOR	
	2000-06-19	FILING DATE	PRIO	
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	2000-03-01	FILING DATE	PRIO	
	2000-02-25	FILING DATE	PRIO	
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	1999-09-30	FILING DATE:	PRIOR	
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	NUMBER: 09/399,723	APPLICATION	PRIOR	
	1999-07-30	II	PRIOR	
	NUMBER: 09/365,164	APPLICATION	PRIOR	
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	NUMBER: 09/342,68/	APPLICATION FILING DATE:	PRIOR	
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	1999-05-14 NUMBER: 09/336	PPLICATION	PRIOR	
	NUMBER: 0		PRIOR	
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	1999-02-26	FILING DATE:	PRIOR	
	NUMBER: 09/259,388	APPLICATION	PRIOR	
	NUMBER: 0	APPLICATION	PRIOR	
	NUMBER: 09/223,546	FILING DATE:	PRIOR	
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	NUMBER: 09/1	APPLICATION	PRIOR	
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Best Local Similarity
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LOCATION: (6)...(761)
-09-796-753-55
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PRIOR APPLICATION NUMBER: 09/605,317
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-09-30
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: 09/606,565
FILING DATE: 2000-06-29
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RESULT 11
US-10-205-823-412
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 412
LENGTH: 1141
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
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                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.7%;
Best Local Similarity 98.4%;
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APPLICANT:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/307,982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: MRI-044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/362,158 FILING DATE: 2002-03-05
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Monahan, John E.
Endege, Wilson O.
Gannavarapu, Manjula
Gorbatcheva, Bella
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                               CTACGCCCGGCCTCGGCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCG
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                                                 CTACGCCCCGCCTCGGCCCACCGACCGCCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCG
                                                                                             AGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCCAGAGCCGCAGGT
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Zhao, Xumei
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Glatt, Karen
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Kamatkar, Shubhangi
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o. US20030108963A1
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Pred. No. 1.9e-184;
0; Mismatches 13;
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APPLICANT: INJUMENT: OCHE IN APPLICANT: BUTGATC, LAWYEGNE J.

FITTLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRE'

FILE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRE'

FILE REFERENCE: MPMO1-029PZRNM

CURRENT APPLICATION NUMBER: US/10/301,822

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 60/339,971

PRIOR PHILING DATE: 2001-12-10

PRIOR FILING DATE: 2001-03-05

PRIOR APPLICATION NUMBER: US 60/361,978

PRIOR APPLICATION NUMBER: US 60/381,988

PRIOR APPLICATION NUMBER: US 60/381,988

PRIOR APPLICATION NUMBER: US 60/381,988

PRIOR FILING DATE: 2002-05-20

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 208

LENGTH: 1141
                       ; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE;
; NAME/KEY: CDS
; LOCATION: (96)...(854)
US-10-301-822-208
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APPLICANT: Millennium Pharmaceuticals,
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 208, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
 Query Match
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Kamatkar, Shubhangi
Schlegel, Robert
Monahan, John E.
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  60.7%;
 Score 802.2;
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Sequence 412, Application US/11051454
Publication No. US20050191673A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarrapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kanatkar, Shubhangi
APPLICANT: Kanatkar, Shubhangi
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                                                                                                                                        RESULT 13
US-11-051-454-412
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CURRENT FILING DATE: 2005-02-04
PRIOR APPLICATION NUMBER: US/10/205,823
PRIOR FILING DATE: 2002-07-25
PRIOR PILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
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SEQ ID NO 412
LENGTH: 1141
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APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
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PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
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"Illiams, P.Mickey

"APPLICANT: Wu, Thomas
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
FILL REFERENCE: PSOLORI-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 44
LENGTH: 1850
TYPE: DN*
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Publication No. US20030148408A1

GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
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Pred. No. 1.9e-184;
0; Mismatches 13;
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TITLE OF INVENTION: TREATMENT OF TUMOR

TITLE OF INVENTION: TREATMENT OF TUMOR

FILE REFERENCE: P5010R1-US

CURRENT APPLICATION NUMBER: US/10/872,972

CURRENT FILING DATE: 2004-06-21

PRIOR APPLICATION NUMBER: US/10/241,220

PRIOR FILING DATE: 2002-09-11

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 44

LENGTH: 1850

TYPE: DNA

ORGANISM: Homo Sapien

US-10-872-972-44
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Publication No. US20040229277A1
GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Baul
APPLICANT: Spencer, Susan
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Williams, P.Mickey
Wu, Thomas
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No. US20040229277A1
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ilarity 98.4%;
Conservative
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Pred. No. 1.9e-184;
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Search completed: February 28, 2006, 15:52:47 Job time: 1248.32 secs

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Title:
Perfect score:
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Listing first 45 summaries
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Sequence 1, Appli	Sequence 550, App	Sequence 3, Appli	Sequence 9329, Ap	Sequence 5000, Ap	Sequence 748, App	Sequence 34, Appl	Sequence 1, Appli	Sequence 35, Appl	Sequence 9, Appli	Sequence 2, Appli	Sequence 21764, A	Sequence 35, Appl	Sequence 9328, Ap	Sequence 9327, Ap	Sequence 543, App	Sequence 192, App	Sequence 6, Appli	Sequence 5, Appli	Sequence 22, Appl	Sequence 532, App	Sequence 7162, Ap	Sequence 13385, A	Sequence 2, Appli	Sequence 2747, Ap

## ALIGNMENTS

PREVENTION, AND  1141;  0; Gaps 0;	Query Match 60.7%; Score 802.2; DB 12; Length 1141; Best Local Similarity 98.4%; Pred. No. 4.5e-160; Matches 810; Conservative 0; Mismatches 13; Indels 0;	WS-11-186-284-208  US-11-186-284-208  Sequence 208, Application US/11186284  Publication No. US20050266493A1  GENERAL INFORMATION:  APPLICANT: Millennium Pharmaceuticals, Inc.  APPLICANT: Millennium Pharmaceuticals, Inc.  APPLICANT: Guillemette, Tracy L.  APPLICANT: Guillemette, Tracy L.  APPLICANT: Monahan, John E.  APPLICANT: Monahan, John E.  APPLICANT: Monahan, John E.  APPLICANT: Monahan, John E.  APPLICANT: Hurgart, Lawrence J.  ITTLE OF INVENTION: MOYEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, ITTLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, ITTLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, ITTLE OF INVENTION NUMBER: US/11/186,284  CURRENT APPLICATION NUMBER: US/10/301,822  PRIOR APPLICATION NUMBER: US/10/301,822  PRIOR APPLICATION NUMBER: US 60/339,971  PRIOR APPLICATION NUMBER: US 60/361,978  PRIOR FILING DATE: 2002-05-20  NUMBER OF SEQ ID NOS: 228  SOCITURE: POWA  ORGANISM: Homo Sapiens  FEATURE:  NAME/KEY: CDS  JAME/KEY: CDS  JAME/K
		PREVENTI

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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, KVUZEt
TITLE OF INVENTION: Bioinformatically detects
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7163
SEQ ID NO 7163
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-10-310-914A-7163/c
                                                                                                                                                                                                                                                                                                                                Sequence 7163, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
TYPE: RNA
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable gro
TITLE OF INVENTION: Bioinformatically detectable gro
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6542
LENGTH: 97
mvor: DNA
                                                                                                  APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable graphic of INVENTION: Bioinformatically detectable graphic of INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1107
LENGTH: 97
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US-10-310-914A-1107/c
; Sequence 1107, Application US/10310914A
; Publication No. US20060003322A1
; Publication No. US20060003322A1
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/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-1107
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; ORGANISM: Human
US-10-310-914A-6542
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US-10-310-914A-6542/c
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US-10-310-914A-7163
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Best Local Similarity
Matches 128; Conserv
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; ORGANISM: Human
US-10-310-914A-1106
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                                                                                                                                                     FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
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Best Local S
Matches 96
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SOFTWARE: Patentin version 3.3
SEQ ID NO 1106
LENGTH: 94
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Matches
                                                                                                              SOPTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5000
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FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hongjin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Michele Cargill APPLICANT: Hongjin Huang
                                                        ORGANISM: Homo sapiens
                                                                                TYPE: DNA
NAME/KEY: misc_feature
LOCATION: 1661, 1662, 1663, 1664, 1665, 1666, 1667, 1668, 1669, 1670.
                                                                                                LENGTH: 16917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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90; Conserv
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95.7%;
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Pred. No. 1.
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LOCATION: 1856, 1857, 1858, 1859,
LOCATION: 1866, 1867, 1868, 1869,
LOCATION: 1876, 1877, 1878, 1879,
LOCATION: 1886, 1887, 1888, 1889,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1817, 1818, 1819, 1820, LOCATION: 1827, 1828, 1829, 1830, LOCATION: 1837, 1838, 1839, 1840, LOCATION: 1847, 1848, 1849, 1850, OTHER INFORMATION: n = A,T,C or G
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LOCATION: 1778, 1779,
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1681, 1682, 1683, 1684,
1691, 1692, 1693, 1694,
ORMATION: n = A,T,C or G
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Pred. No. 9.7e-06;
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RESULT 8
US-09-925-065A-92367/c
; Sequence 92367, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
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US-11-052-554A-529
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APPLICANT: Sachdeva, et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

FILE REFERENCE: 30653/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR PRIOR PILING DATE: 2004-07-20

PRIOR PILING DATE: 2004-07-20

RENOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTMARE: Patentin version 3.3
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                 FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Mycobacterium tuberculosis H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 3240
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49.8%;
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Pred. No. 1.2e-05;
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; LOCATION: (1)...(2600)
; OTHER INFORMATION: n =
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR TILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 92367
LENGTH: 2600
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                                                                  GCCTCCCCGCCGCGCCTCCTG---CATGCGGGGCCCCAGCTCCGGGCGCCGGGA
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CCGGGCGTCGGCGTCGGGGAGAGCCCGTCCTCCCCGCGTGGCG
                               CACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGC
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49.6%;
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Pred. No. 1.6e-05;
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Sequence 37513/c

Sequence 37513, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.
ITILE OF INVENTION: Identification and Mapping of Single
ITILE OF INVENTION: Nucleotide Polymorphisms in the Human General Physics of Structure 10827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/252,065

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-16

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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 37513 LENGTH: 1608

PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2001-05-05 NUMBER OF SEQ ID NOS: 957086

60/289,846

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                                     ; ORGANISM: Homo sapiens 
US-09-925-065A-37514
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Best Local Similarity
Matches 200; Conserv
                                                                                                         SOFTWARE: Fast
SEQ ID NO 37514
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37514, Application US/09925065A Publication No. US20040181048A1
Query Match
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
                                                                                                                                                                                                PRIOR FILING DATE: 2000-10-24
FRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/243,096 PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/925,065A
                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 108827.135
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ORGANISM: Homo sapiens
                                                                                                                                                              APPLICATION NUMBER: US 60/289,846 FILING DATE: 2001-05-09
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                                                                                                                              FastSEQ for Windows Version 4.0
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 5.1%;
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Pred. No. 2.9e-
0; Mismatches
   Score
 67;
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 Length 1608;
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RESULT 11
US-09-25-065A-37515/c
; Sequence 37515, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-37515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTS:
SEQ ID NO 37515
FENGTH: 1608
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                                                                                                                                                                                                                                                              Query Match 5.1%;
Best Local Similarity 49.6%;
Matches 200; Conservative
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
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0; Mismatches 200;
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US-09-925-065A-92368/c
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US-09-925-065A-92368
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PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR TILING DATE: 2000-11-20

PRIOR PPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR TILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR PILING DATE: 2001-05-09

PRIOR FILING DATE: 2001-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version SEQ ID NO 92368 LENGTH: 2600
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Mulleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
NAME/KEY: misc_feature LOCATION: (1)...(2600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
1242
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Pred. No. 2.9e-05;
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US-11-052-554A-529/c
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0; Mismatches 255
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RESULT 14
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              Sequence 2, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
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Best Local
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
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CURRENT FILING DATE: 2005-02-07
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  RIOR APPLICATION NUMBER:
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pred. No. 5.1e-05;
0; Mismatches 207;
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NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                 207;
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                                                                                                                                                                                                                    GCTGCGGCGCCCGAGGGGGCGTCCTCCGGGCGGGCGGGCTGTGGCCGCCCCCCGCGGGGC
                                                                                                                                                                                                                                             AGCCCCGGCGGCAGCGCGCGCGCCCGCTGCCAGCCCATTTTCCGGACGCCACCCGCGGGCA 174
GGCATGTCGGCGGCGTGGCGTGCGTTACTTCGCCGCCGACG
                                                     TCCGGTGCGTCAGGACGCGTCAGGCGGGGGGGGCGAGCGCGAGCGCGGGGCGTCGGCGGCG
                                                                                                                                                                                      CCGCGCACTGAGCCCCGCGCGCCCCCGGGAACTTGGCGGCGACCCCGAGCCCGGCGAGCCC
                                                                                                                                                                                                                                                                                                                                                     TCCATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                               5.0%;
                                                                                                                                                                                                                                                                                                                                                                                   Score 65.6; DE
Pred. No. 5.5e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               5.5e-05
                                                                                                                                                                                                                                                                                                                                                                                                             DB 12;
                                                                                                                                                                                                                                                                                                                                                                                    194;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Length 191684;
    144860
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Search completed: February 28, 2006, 10:28:36 Job time: 1733.47 secs

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